wwPDB EM Validation Summary Report

May 12, 2025 – 01:32 AM JST

PDB ID	:	8ZGR / pdb_00008zgr
EMDB ID	:	EMD-60088
Title	:	80S ribosome with A/A tRNA and mRNA of WNV
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2024-05-09
Resolution	:	2.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

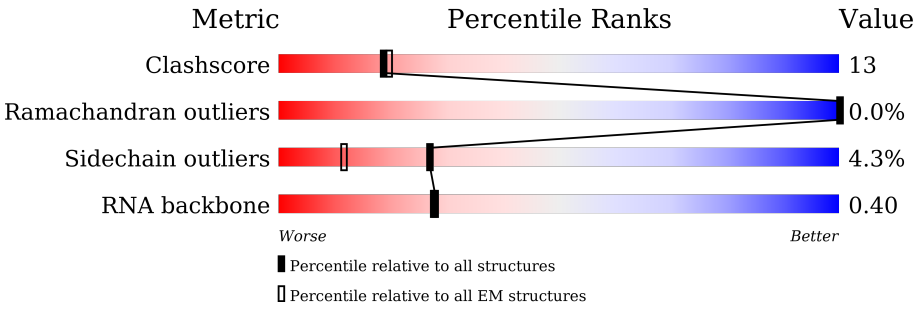
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	LA	3393	9% 46% 40% 8% 6%
2	LB	121	50% 40% 10%
3	LC	158	5% 37% 53% 9%
4	LD	251	65% 31%
5	LE	386	72% 28%
6	LF	361	65% 34%
7	LG	294	11% 65% 34%

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Mol	Chain	Length	Quality of chain
8	LH	175	12% 67% 26% 5%
9	LI	222	75% 25%
10	LJ	233	12% 68% 31%
11	LK	191	5% 57% 38% 5%
12	LL	218	9% 56% 41%
13	LM	169	18% 54% 42%
14	LN	193	6% 72% 26%
15	LO	136	5% 69% 29%
16	LP	203	65% 34%
17	LQ	197	68% 30%
18	LR	183	9% 79% 20%
19	LS	185	66% 34%
20	LT	188	15% 73% 27%
21	LU	171	68% 28%
22	LV	159	5% 65% 31%
23	LW	100	16% 71% 27%
24	LX	136	68% 31%
25	LY	65	69% 31%
26	LZ	121	69% 28%
27	La	125	66% 31%
28	Lb	135	5% 68% 30%
29	Lc	148	69% 28%
30	Ld	58	66% 33%
31	Le	96	69% 29%
32	Lf	109	11% 72% 28%

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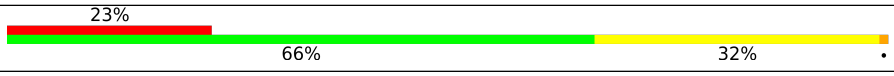
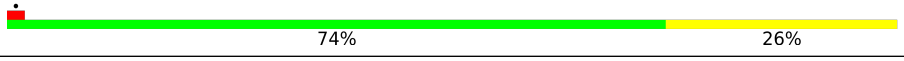
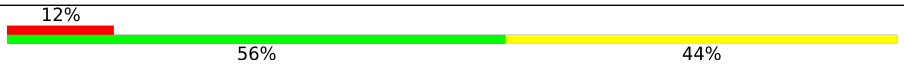
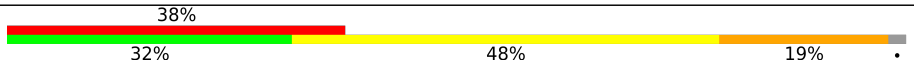
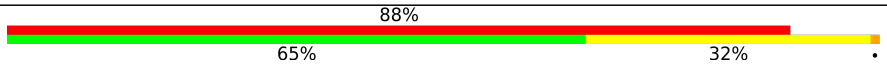
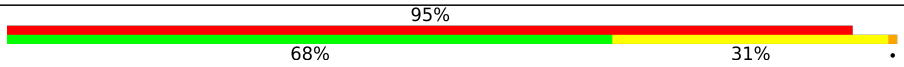
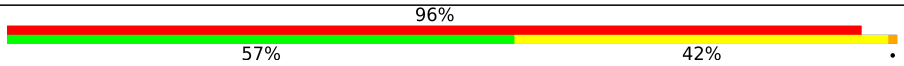
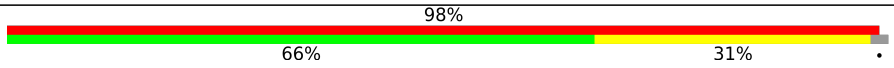
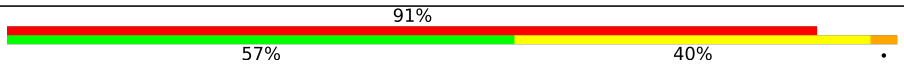
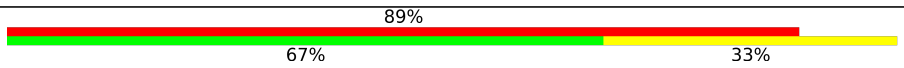
Mol	Chain	Length	Quality of chain
33	Lg	127	
34	Lh	106	
35	Li	112	
36	Lj	119	
37	Lk	99	
38	Ll	81	
39	Lm	77	
40	Ln	50	
41	Lo	52	
42	Lp	25	
43	Lq	103	
44	Lr	91	
45	S2	1800	
46	SA	223	
47	SB	206	
48	SC	92	
49	SD	124	
50	SE	117	
51	SF	141	
52	SG	125	
53	SH	145	
54	SI	143	
55	SJ	101	
56	SK	82	
57	SL	63	

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Mol	Chain	Length	Quality of chain
58	SM	53	68% 62% 36%
59	SN	73	99% 84% 16%
60	SO	312	99% 65% 34%
61	SP	206	54% 53% 42%
62	SQ	232	73% 54% 41%
63	SR	217	38% 59% 38%
64	SS	260	38% 52% 45%
65	ST	228	59% 64% 34%
66	SU	185	62% 51% 46%
67	SV	199	17% 57% 35% 6%
68	SW	185	58% 61% 39%
69	SX	146	14% 64% 31%
70	SY	150	23% 61% 37%
71	SZ	128	85% 60% 36%
72	Sa	87	46% 59% 39%
73	Sb	129	7% 57% 40%
74	Sc	144	15% 68% 31%
75	Sd	134	62% 63% 37%
76	Se	97	36% 65% 34%
77	Sf	81	47% 70% 30%
78	Sg	57	67% 67% 33%
79	Ta	77	99% 32% 49% 18%

2 Entry composition (i)

There are 79 unique types of molecules in this entry. The entry contains 200681 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA (3393-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	LA	3184	68091	30415	12259	22233	3184	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	?	-	G	deletion	GB 2209526103

- Molecule 2 is a RNA chain called 5S rRNA (121-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	LB	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA (158-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	LC	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LD	251	1899	1182	385	331	1	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LE	386	3075	1950	584	533	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	LH	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LN	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 15 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 16 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LR	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	LT	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	LW	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 24 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 25 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	65	Total	C	N	O	S	0	0
			528	339	104	84	1		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 27 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	La	125	Total 984	C 620	N 191	O 173	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Lb	135	Total 1080	C 701	N 199	O 180	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	148	Total 1169	C 747	N 231	O 188	S 3	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Ld	58	Total 462	C 289	N 100	O 73	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	96	Total 737	C 476	N 123	O 137	S 1	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	109	Total 876	C 556	N 167	O 152	S 1	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	127	Total 1017	C 644	N 205	O 167	S 1	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	106	Total 850	C 540	N 165	O 144	S 1	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	112	Total 880	C 545	N 179	O 152	S 4	0	0

- Molecule 36 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	119	Total 969	C 615	N 186	O 167	S 1	0	0

- Molecule 37 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	99	Total 766	C 478	N 154	O 132	S 2	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	81	Total 645	C 393	N 141	O 106	S 5	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Lm	77	Total 612	C 391	N 115	O 106	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ln	50	Total 436	C 272	N 97	O 65	S 2	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 42 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lp	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lq	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lr	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 45 is a RNA chain called chain 2 18S rRNA (1800-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 46 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 47 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 48 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SC	92	Total 752	C 487	N 122	O 141	S 2	0	0

- Molecule 49 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	121	Total 875	C 551	N 153	O 169	S 2	0	0

- Molecule 50 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	117	Total 916	C 583	N 171	O 155	S 7	0	0

- Molecule 51 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	SF	141	Total 1105	C 708	N 203	O 194	0	0

- Molecule 52 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	121	Total 948	C 596	N 179	O 171	S 2	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SH	145	Total 1188	C 741	N 237	O 208	S 2	0	0

- Molecule 54 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	143	Total 1112	C 694	N 208	O 208	S 2	0	0

- Molecule 55 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SK	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 57 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 58 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SM	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 59 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SN	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 60 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 61 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 62 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 63 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 64 is a protein called Small ribosomal subunit protein eS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 65 is a protein called Small ribosomal subunit protein eS6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 66 is a protein called Small ribosomal subunit protein eS7A.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	SU	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 67 is a protein called Small ribosomal subunit protein eS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 68 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 69 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 70 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 71 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 72 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 73 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 74 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 75 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	Sd	134	Total	C	N	O	0	0
			1032	651	195	186		

- Molecule 76 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 77 is a protein called Small ribosomal subunit protein eS27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 78 is a protein called Small ribosomal subunit protein eS30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	57	Total	C	N	O	S	0	0
			451	284	93	73	1		

- Molecule 79 is a RNA chain called tRNA (77-MER).

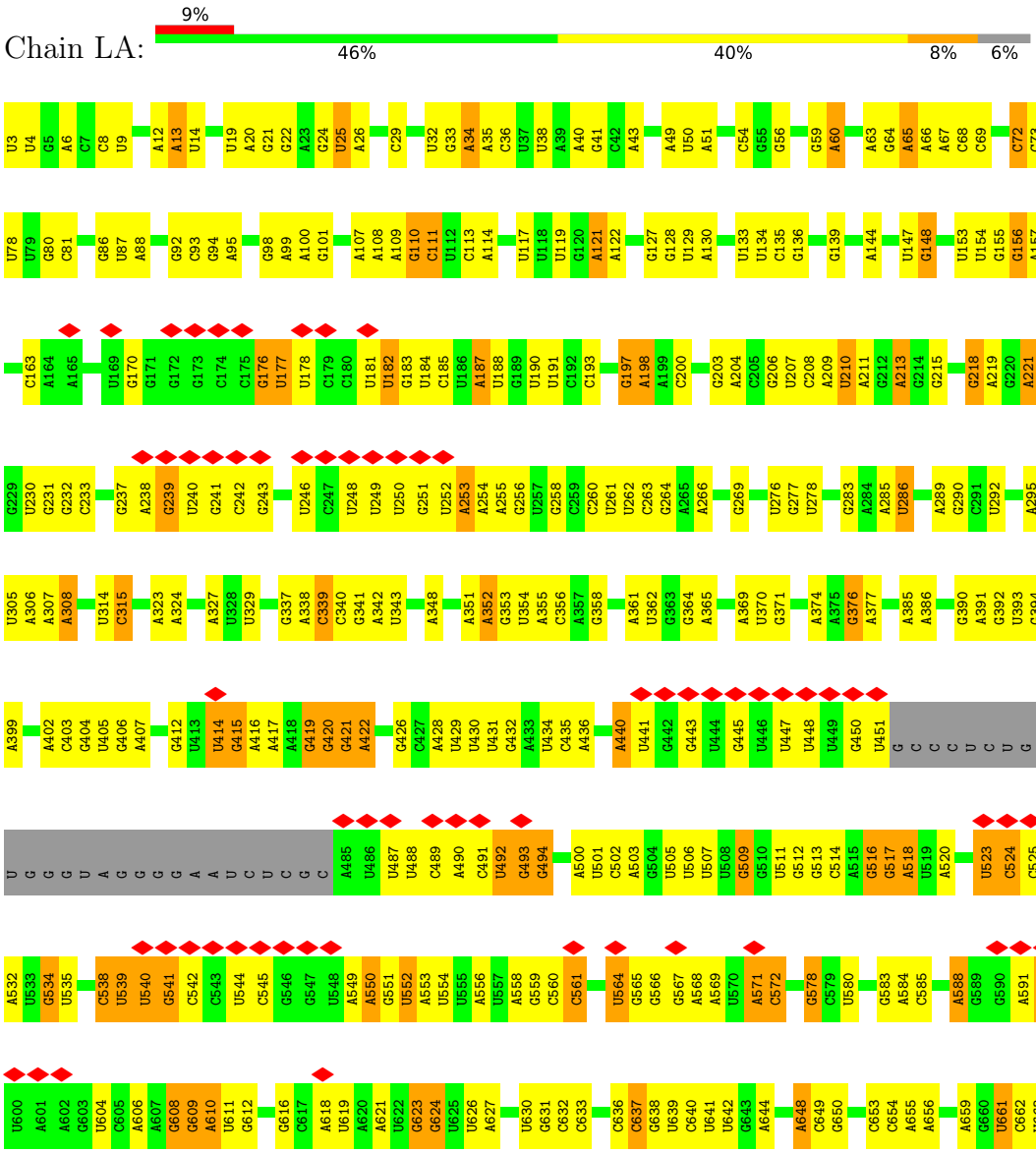
Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ta	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

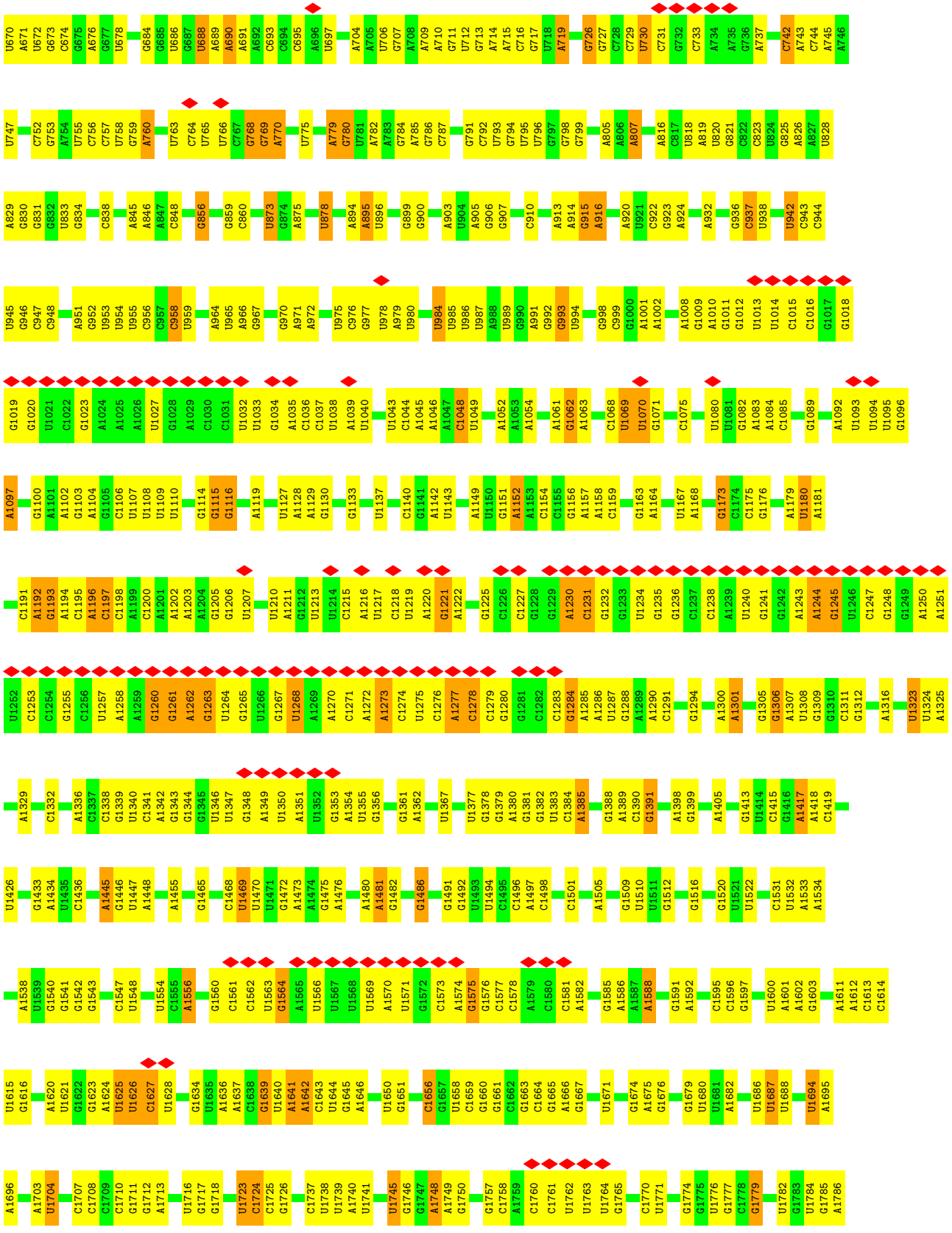
3 Residue-property plots (i)

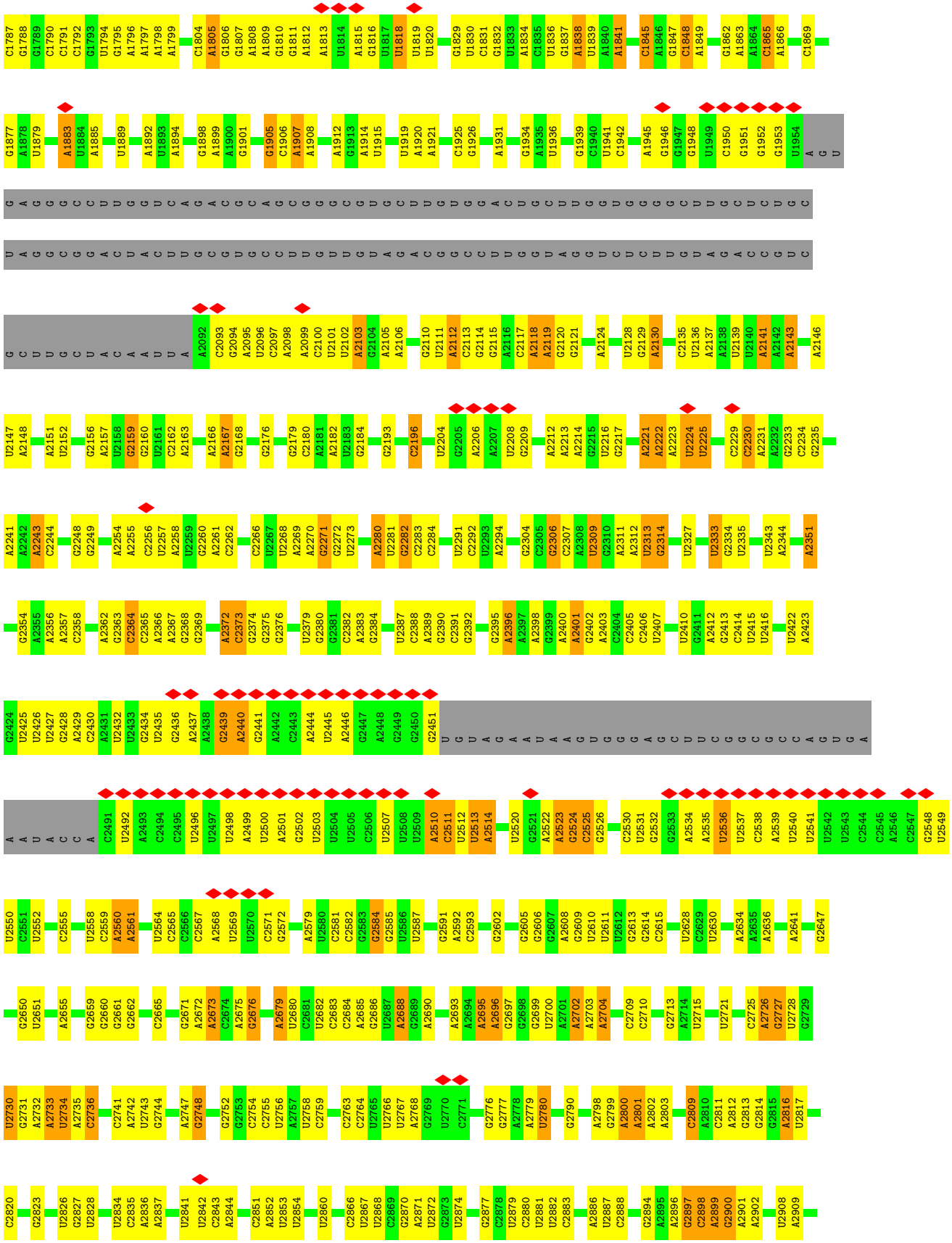
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

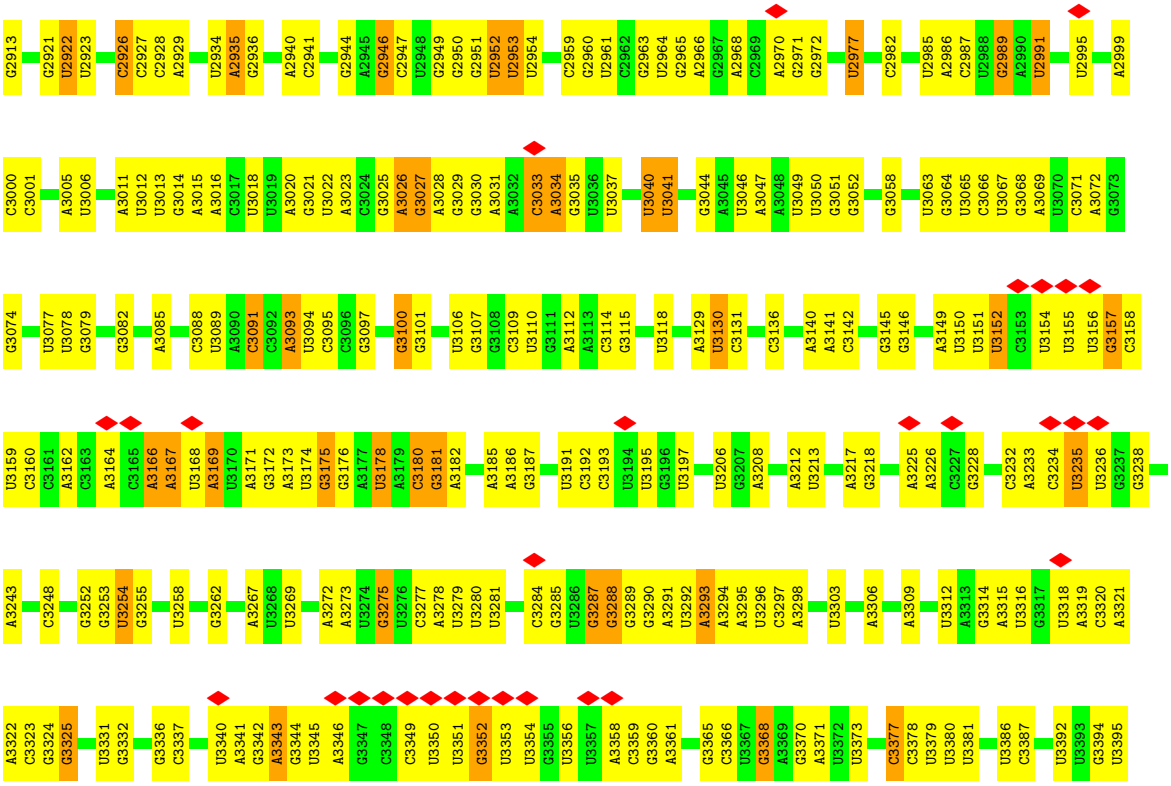
- Molecule 1: 25S rRNA (3393-MER)

Chain LA:



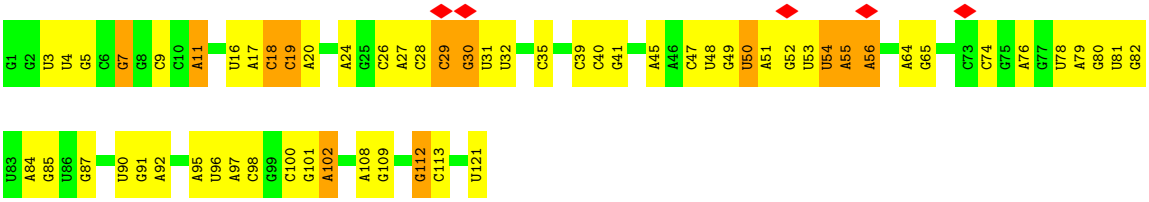






• Molecule 2: 5S rRNA (121-MER)

Chain LB:

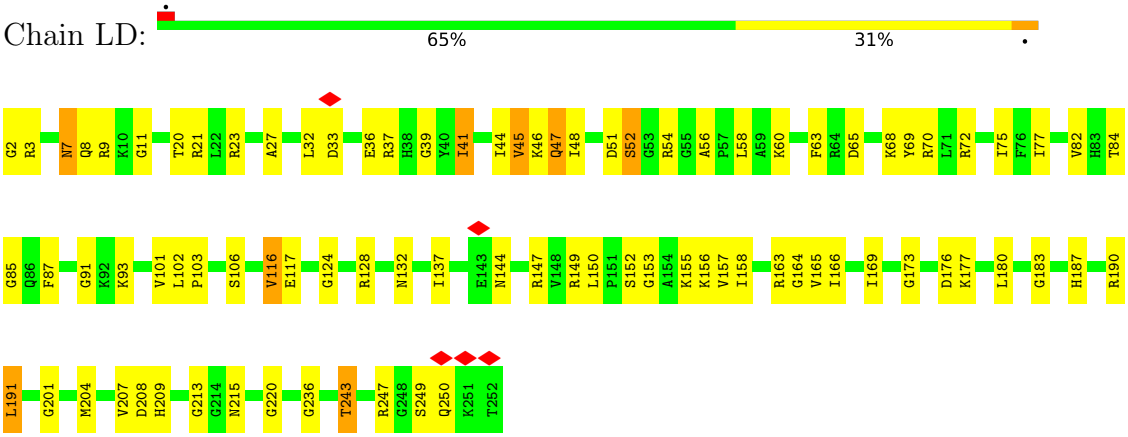


• Molecule 3: 5.8S rRNA (158-MER)

Chain LC:

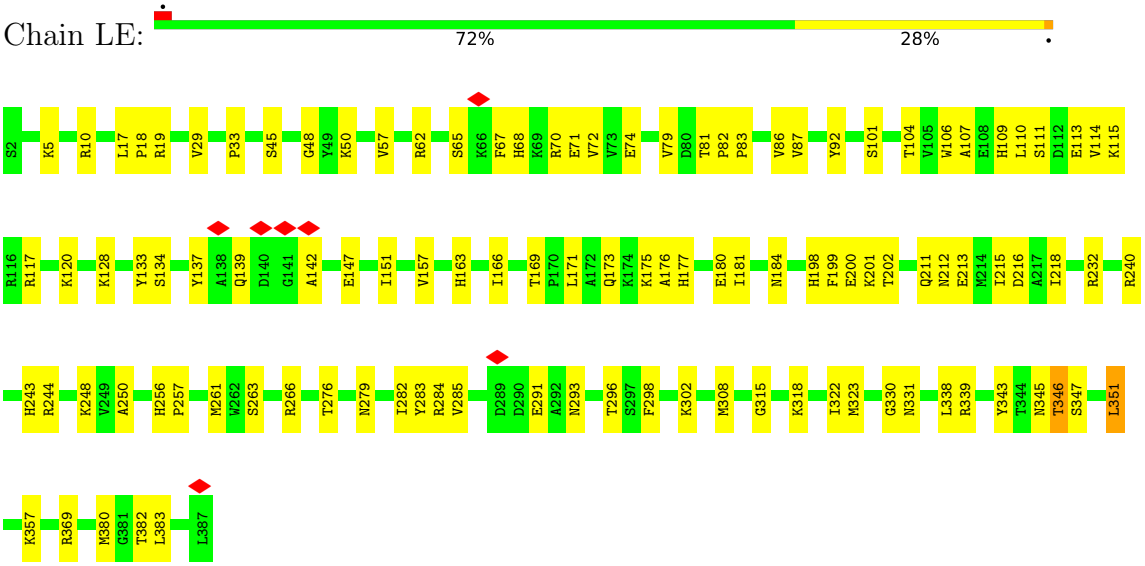
• Molecule 4: Large ribosomal subunit protein uL2A

Chain LD:



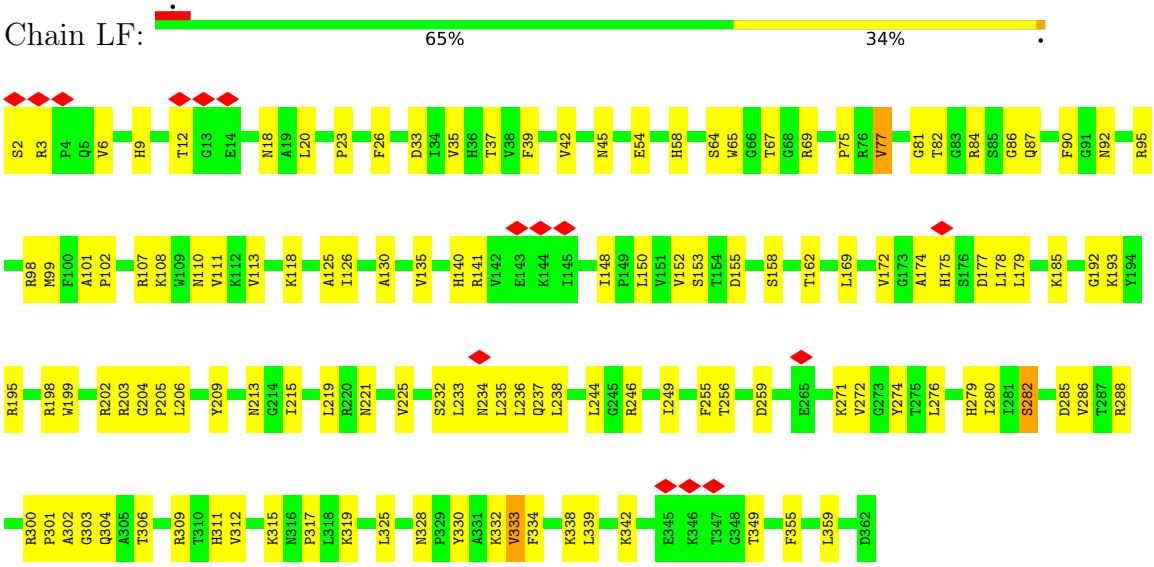
• Molecule 5: Large ribosomal subunit protein uL3

Chain LE:



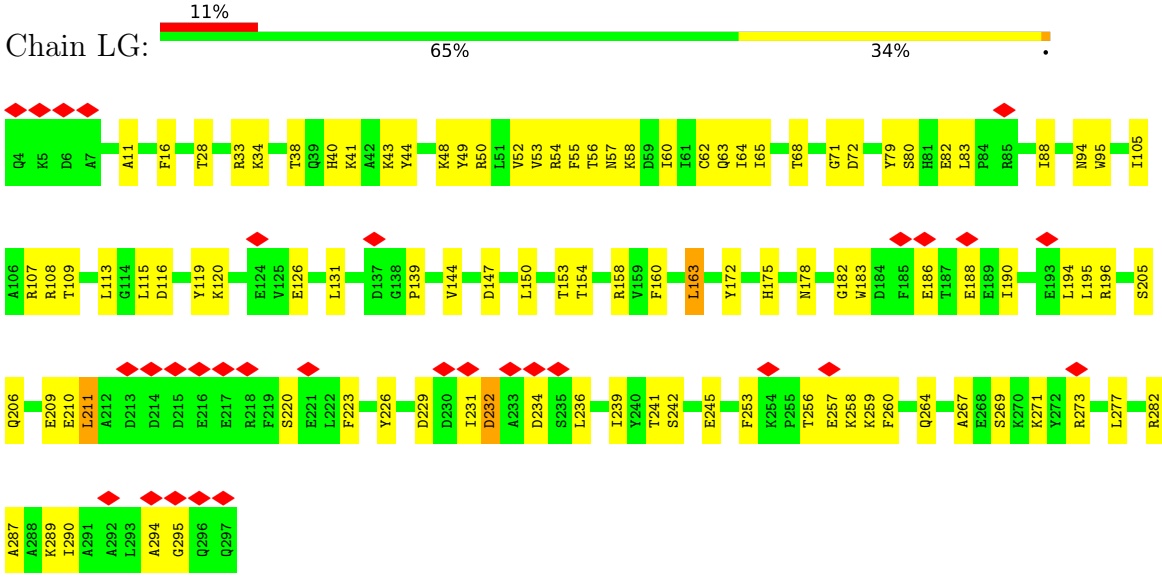
• Molecule 6: Large ribosomal subunit protein uL4A

Chain LF:



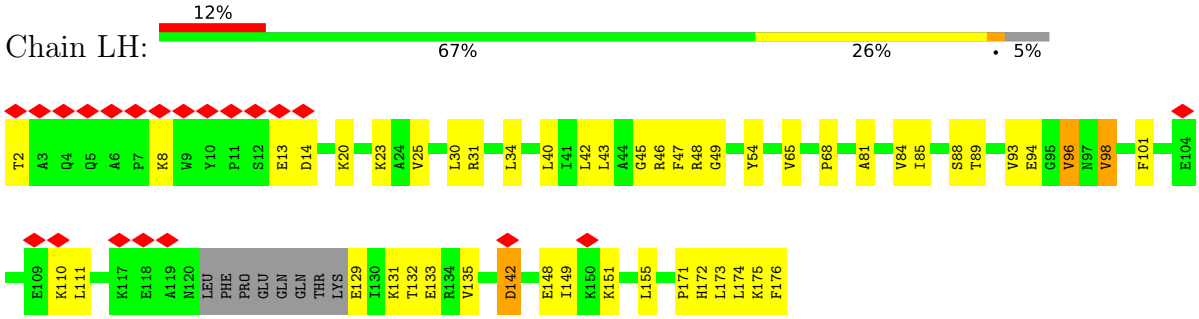
• Molecule 7: Large ribosomal subunit protein uL18

Chain LG:



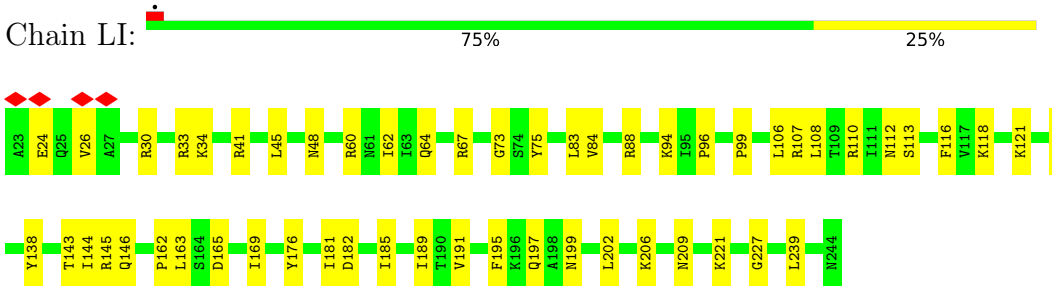
• Molecule 8: Large ribosomal subunit protein eL6B

Chain LH:



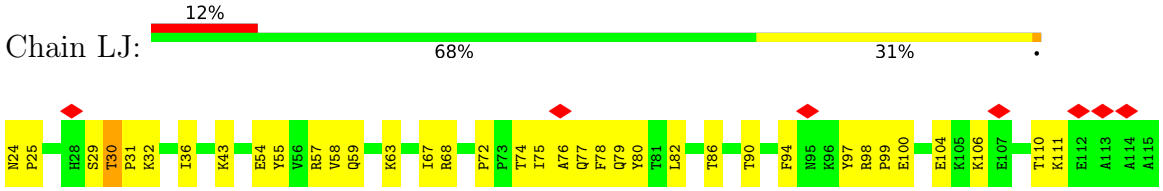
• Molecule 9: Large ribosomal subunit protein uL30A

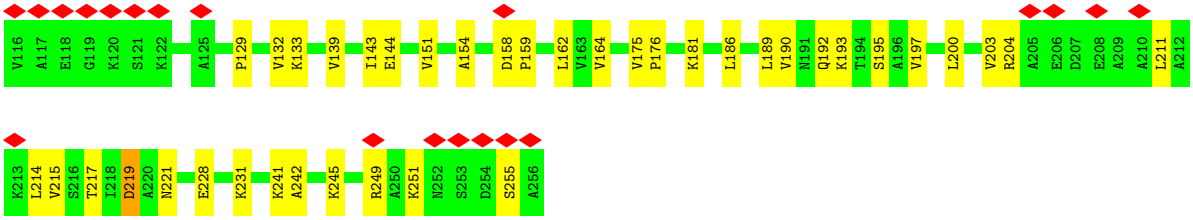
Chain LI:



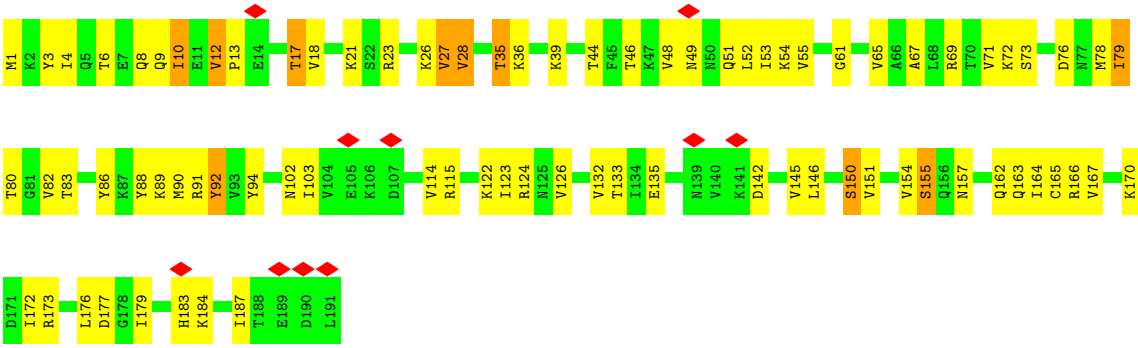
• Molecule 10: Large ribosomal subunit protein eL8A

Chain LJ:

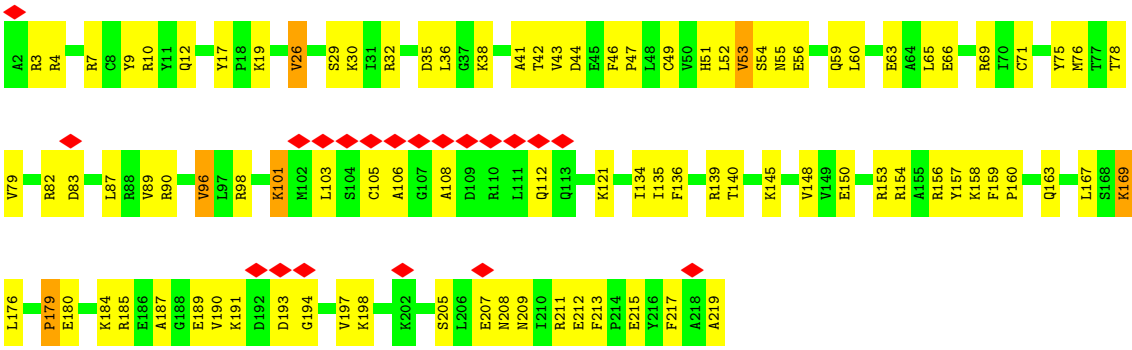




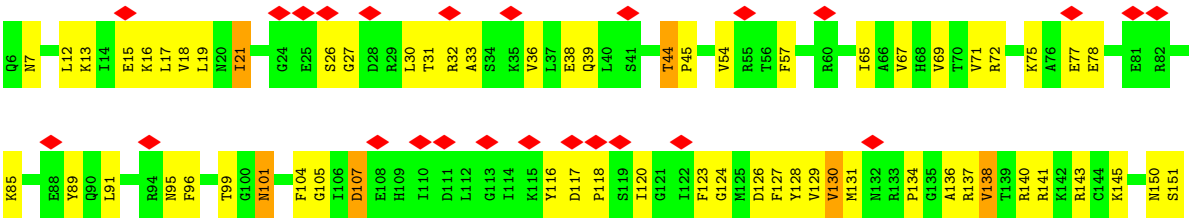
• Molecule 11: Large ribosomal subunit protein uL6A

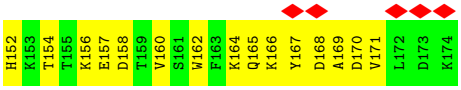


• Molecule 12: Large ribosomal subunit protein uL16

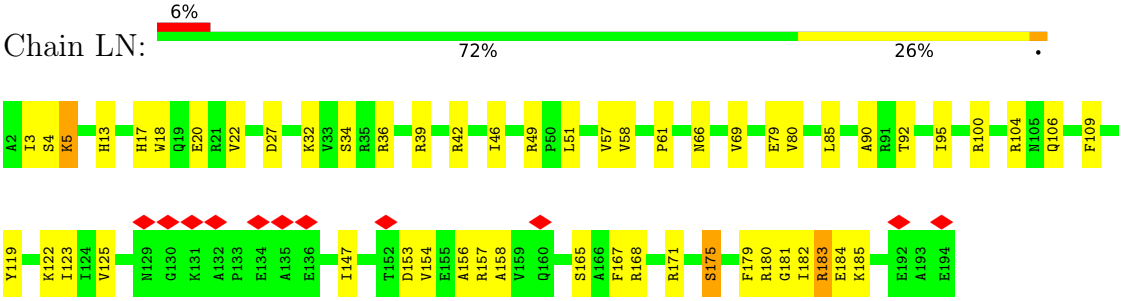


• Molecule 13: Large ribosomal subunit protein uL5B

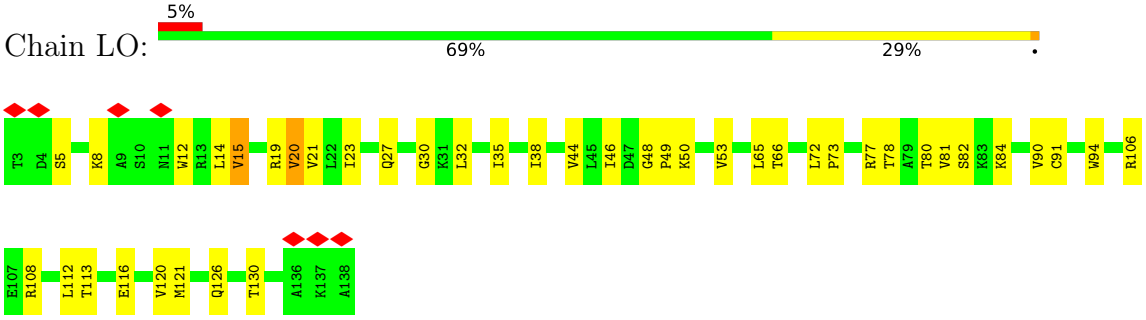




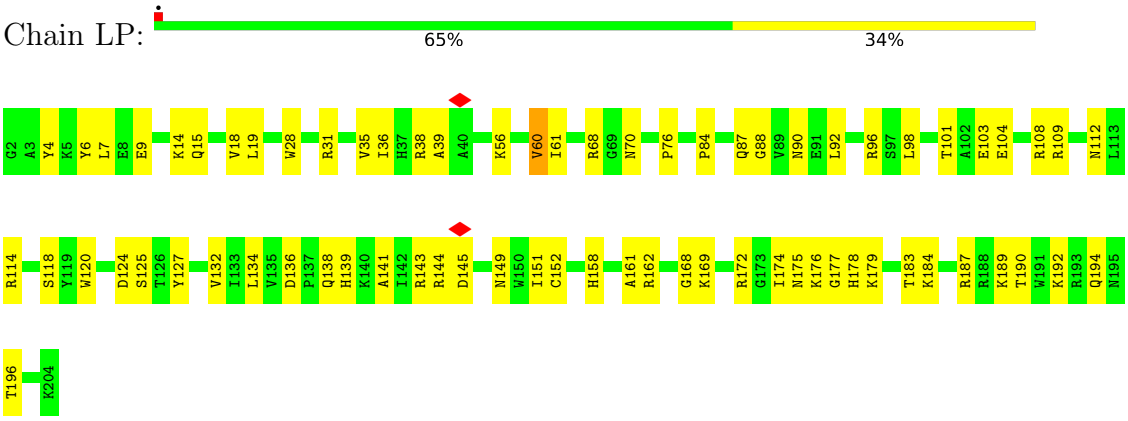
• Molecule 14: Large ribosomal subunit protein eL13A



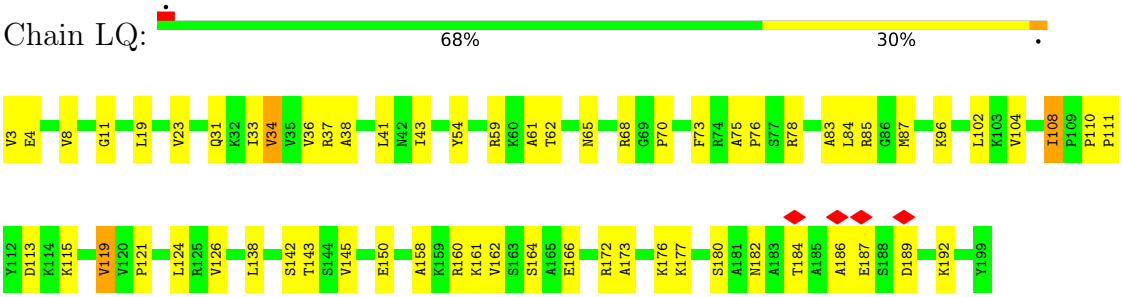
• Molecule 15: Large ribosomal subunit protein eL14A



• Molecule 16: Large ribosomal subunit protein eL15A

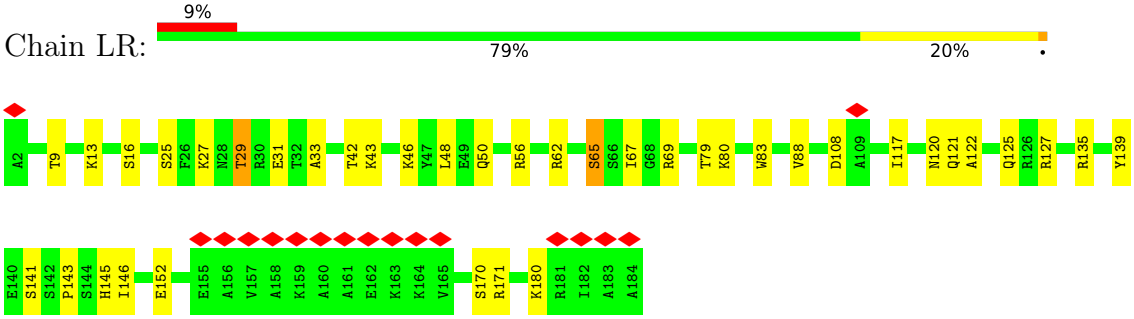


• Molecule 17: Large ribosomal subunit protein uL13A



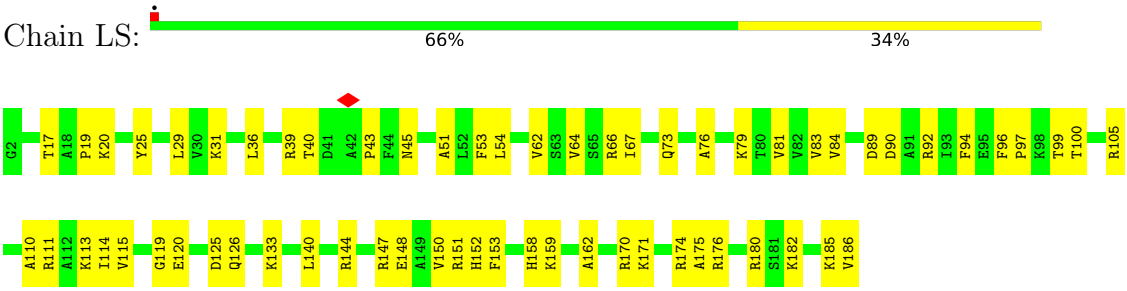
• Molecule 18: Large ribosomal subunit protein uL22A

Chain LR:



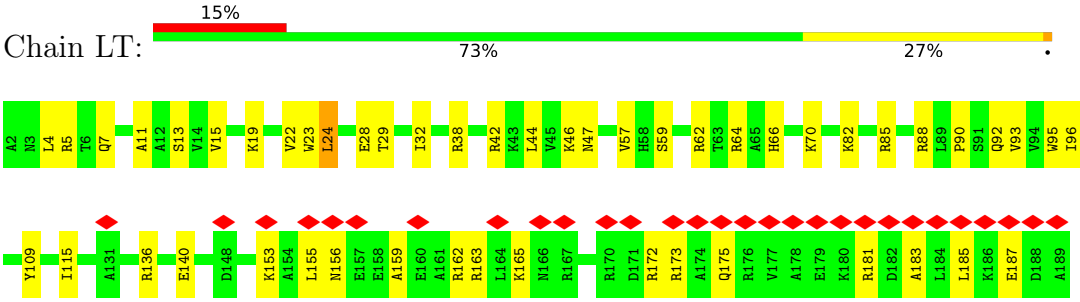
• Molecule 19: Large ribosomal subunit protein eL18A

Chain LS:



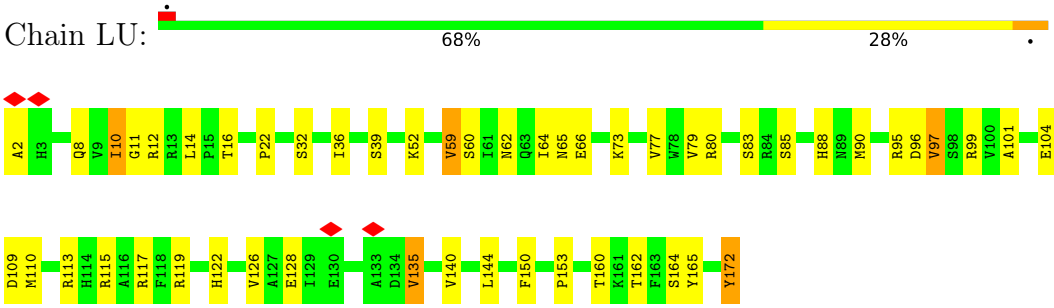
• Molecule 20: Large ribosomal subunit protein eL19A

Chain LT:



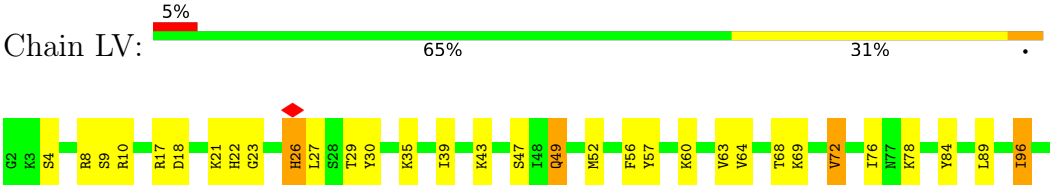
• Molecule 21: Large ribosomal subunit protein eL20A

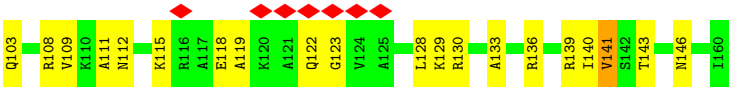
Chain LU:



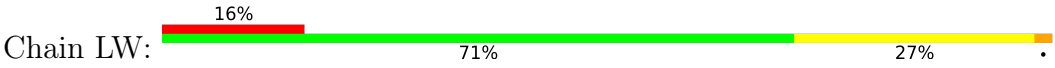
• Molecule 22: Large ribosomal subunit protein eL21A

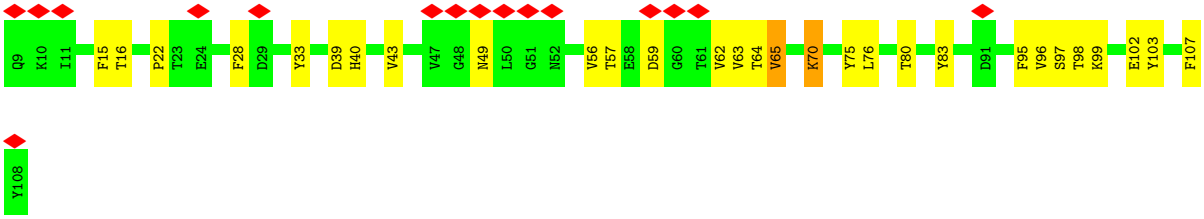
Chain LV:



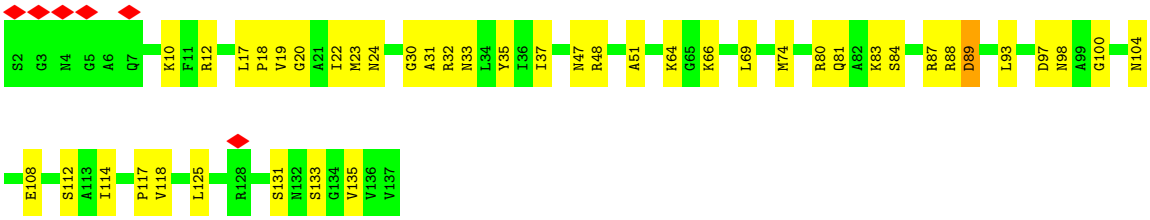


• Molecule 23: Large ribosomal subunit protein eL22A

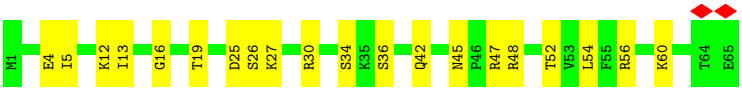




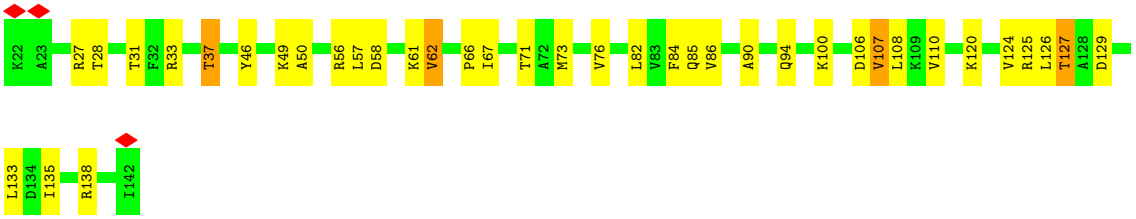
• Molecule 24: Large ribosomal subunit protein uL14A



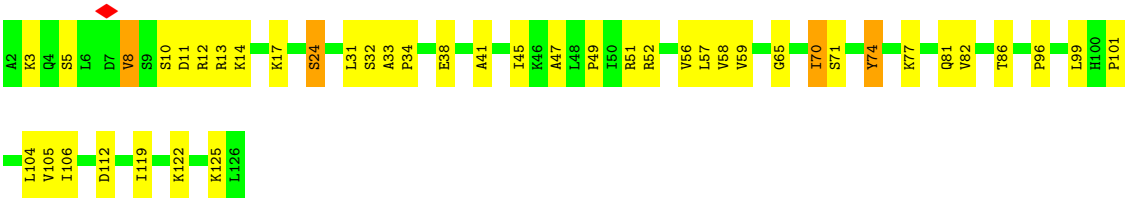
• Molecule 25: Large ribosomal subunit protein eL24A



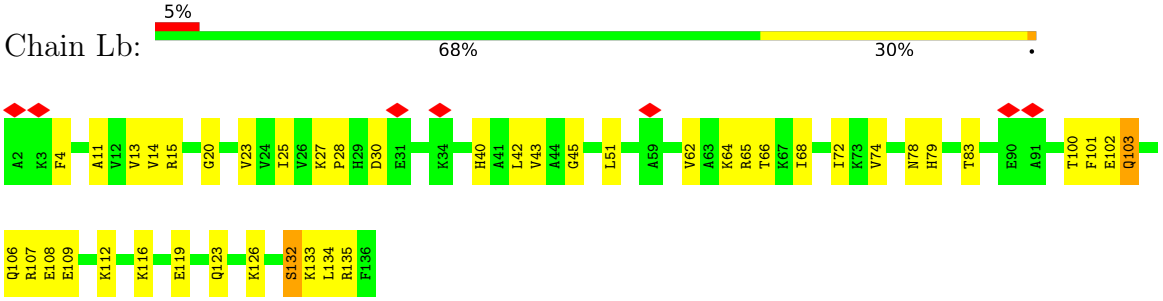
• Molecule 26: Large ribosomal subunit protein uL23



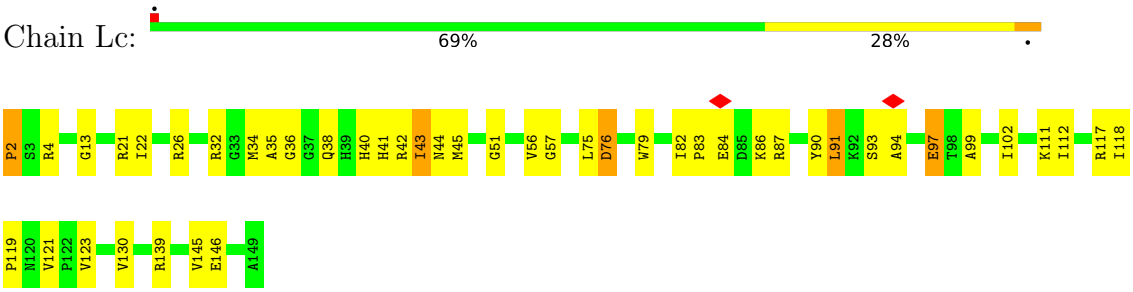
• Molecule 27: Large ribosomal subunit protein uL24A



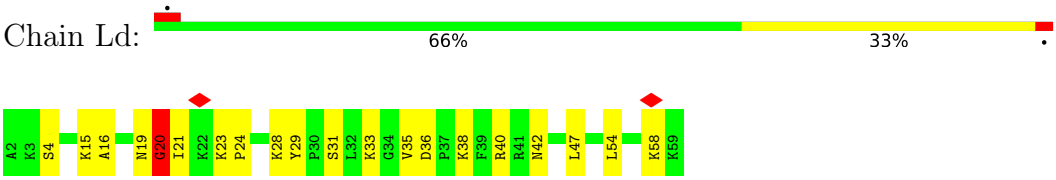
• Molecule 28: Large ribosomal subunit protein eL27A



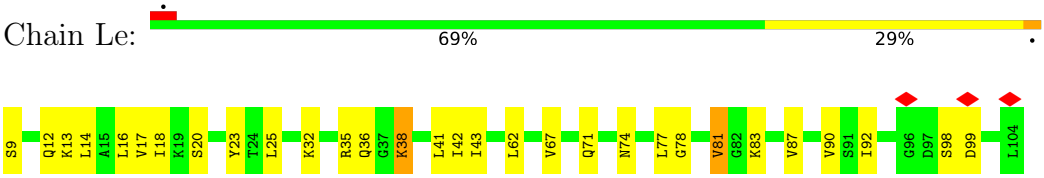
• Molecule 29: Large ribosomal subunit protein uL15



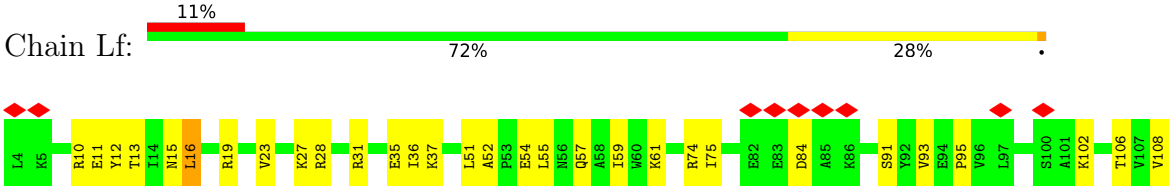
• Molecule 30: Large ribosomal subunit protein eL29



• Molecule 31: Large ribosomal subunit protein eL30

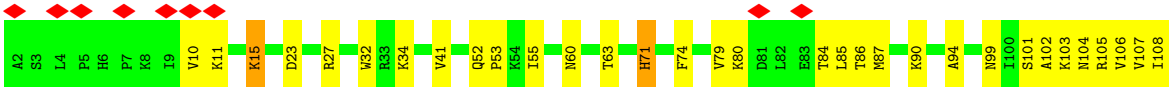


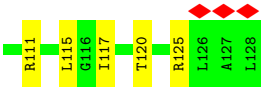
• Molecule 32: Large ribosomal subunit protein eL31A



• Molecule 33: Large ribosomal subunit protein eL32

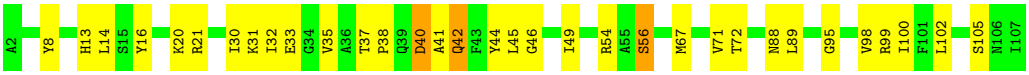
Chain Lg:





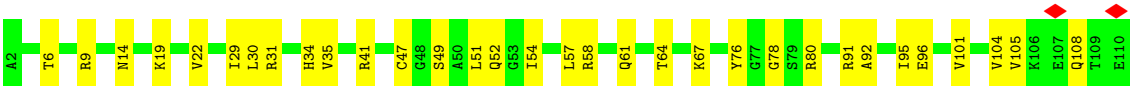
• Molecule 34: Large ribosomal subunit protein eL33A

Chain Lh:



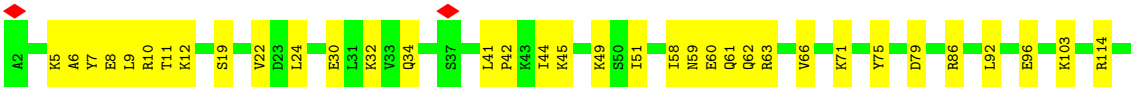
• Molecule 35: Large ribosomal subunit protein eL34A

Chain Li:



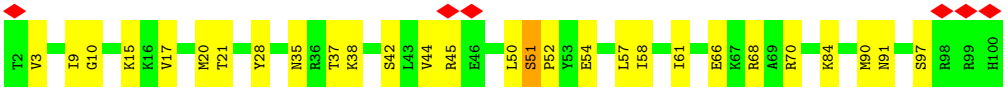
• Molecule 36: Large ribosomal subunit protein uL29A

Chain Lj:

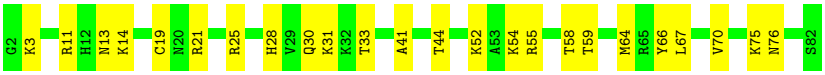


• Molecule 37: Large ribosomal subunit protein eL36A

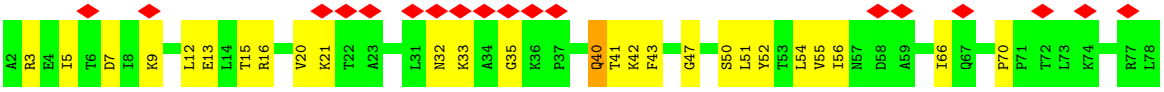
Chain Lk:



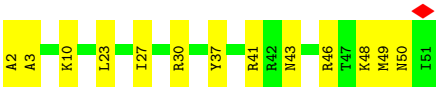
• Molecule 38: Large ribosomal subunit protein eL37A



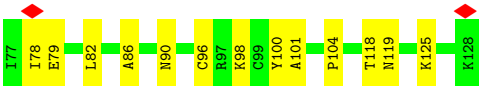
• Molecule 39: Large ribosomal subunit protein eL38



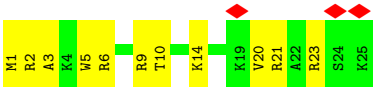
• Molecule 40: Large ribosomal subunit protein eL39



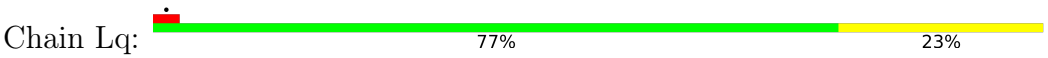
• Molecule 41: Large ribosomal subunit protein eL40A



• Molecule 42: Large ribosomal subunit protein eL41A

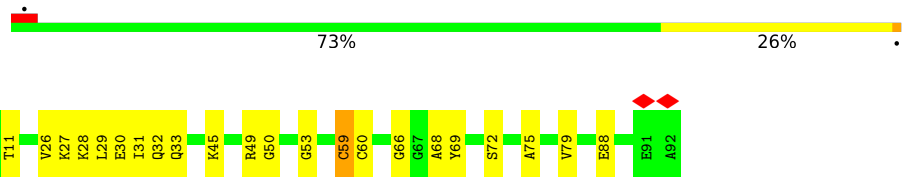


• Molecule 43: Large ribosomal subunit protein eL42A



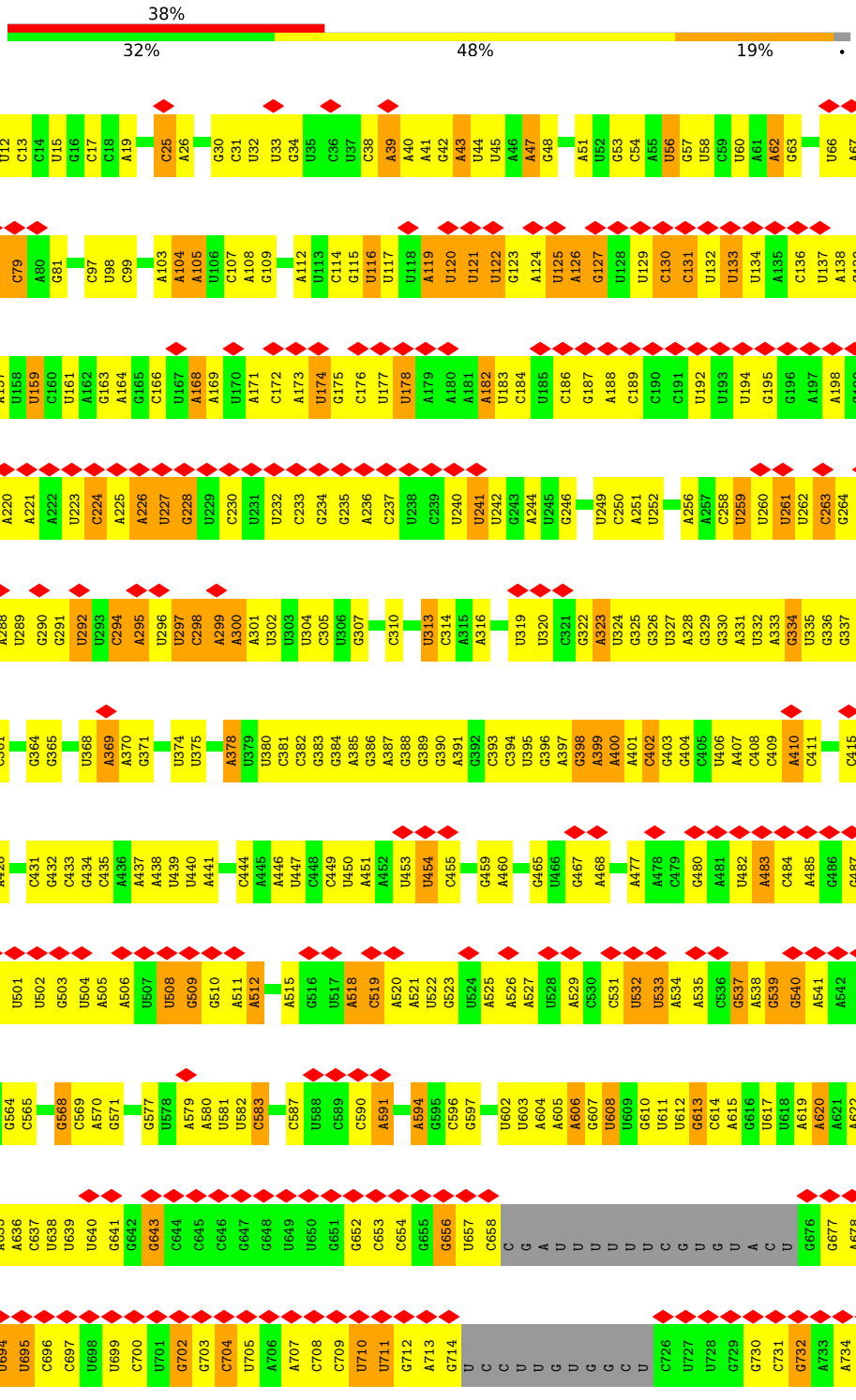
• Molecule 44: Large ribosomal subunit protein eL43A

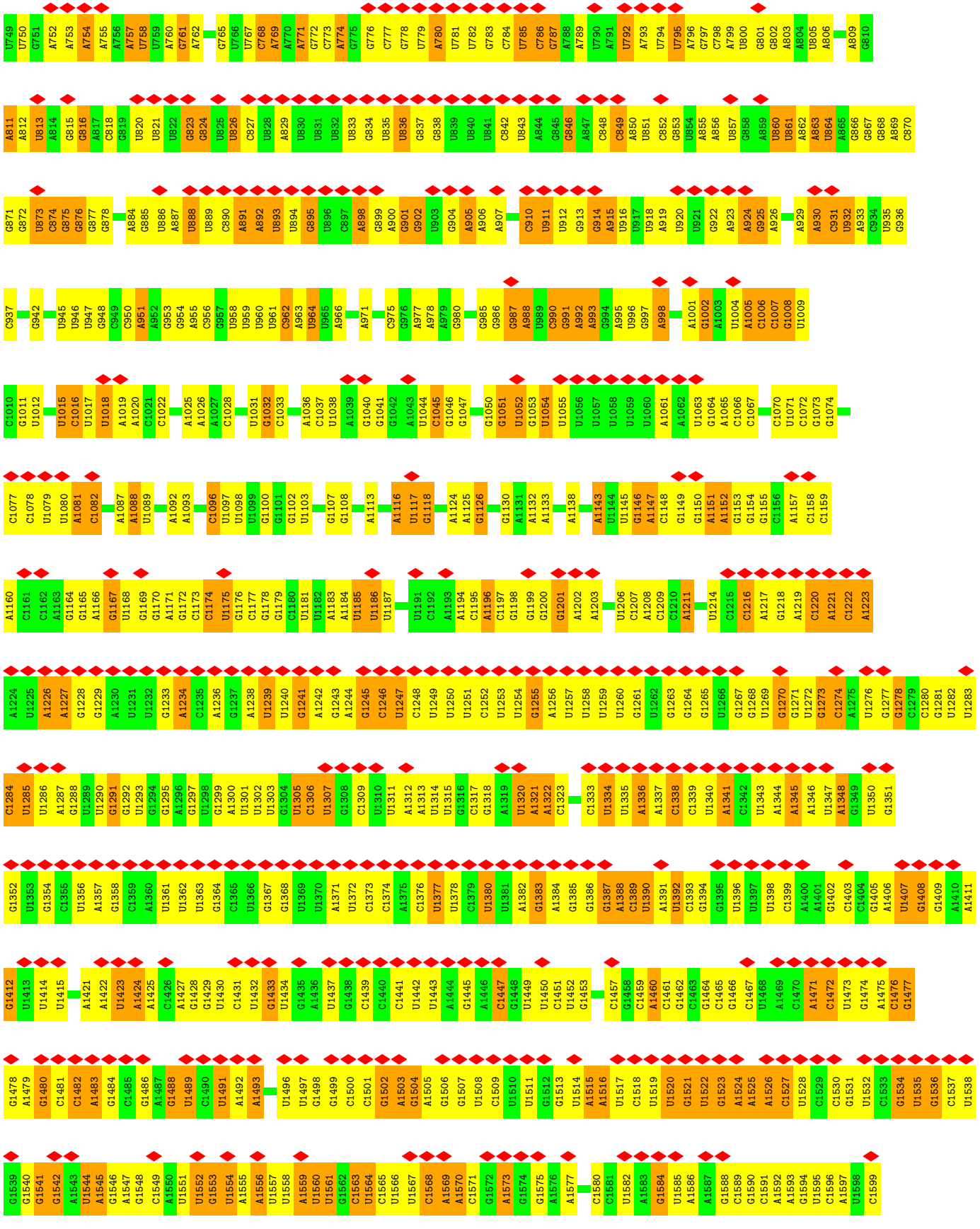
Chain Lr:

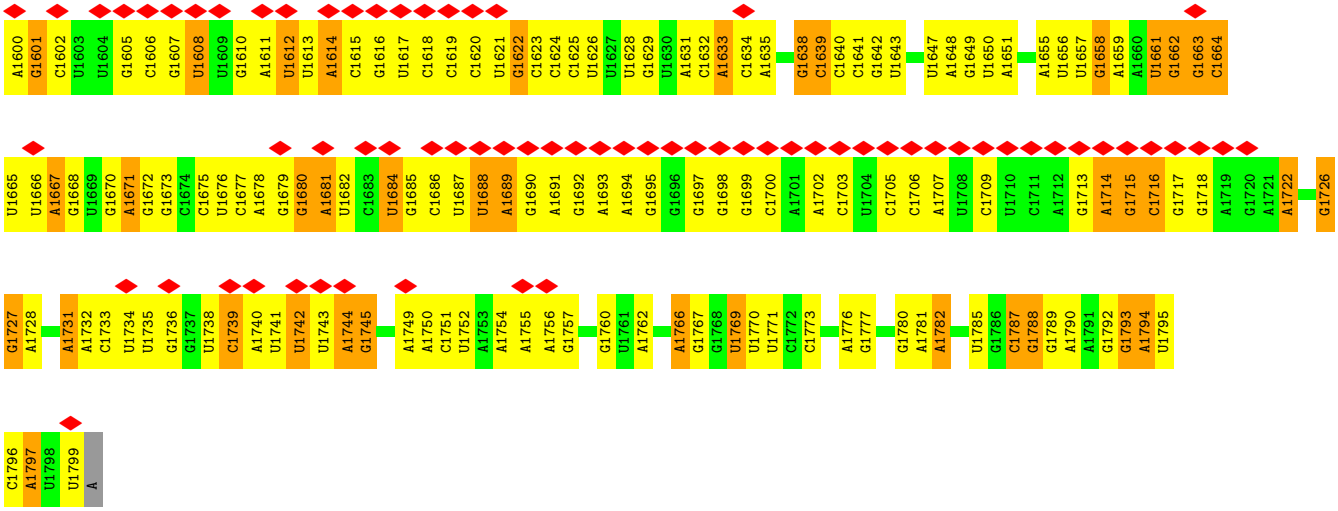


• Molecule 45: chain 2 18S rRNA (1800-MER)

Chain S2:

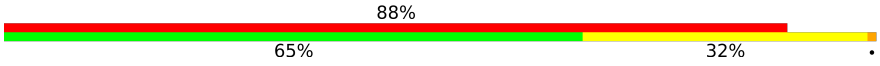


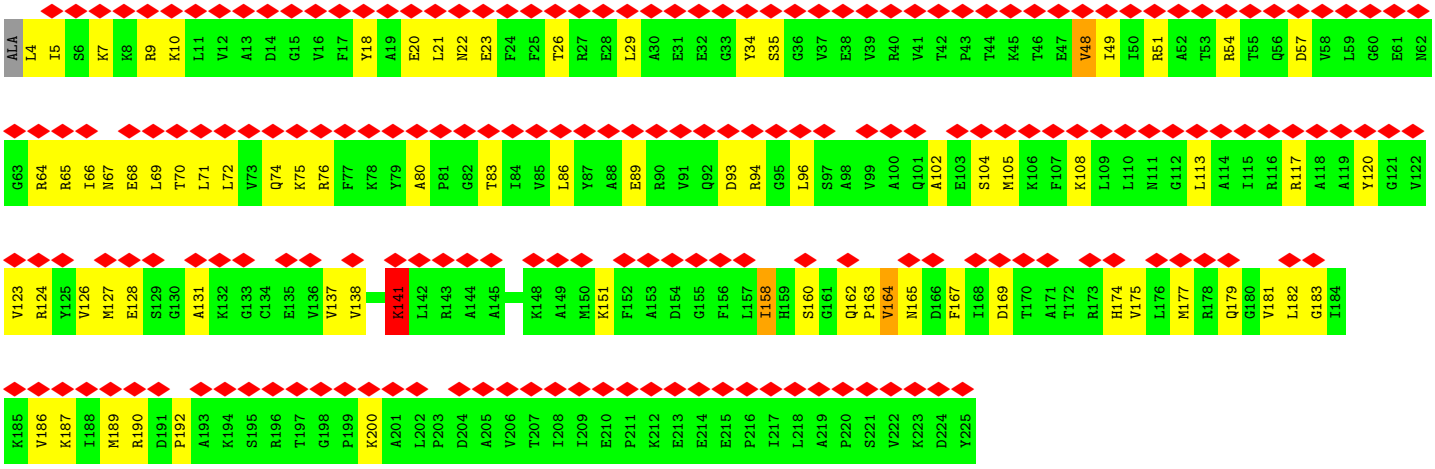




• Molecule 46: Small ribosomal subunit protein uS3

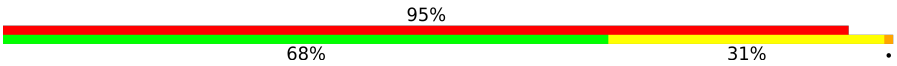
Chain SA:

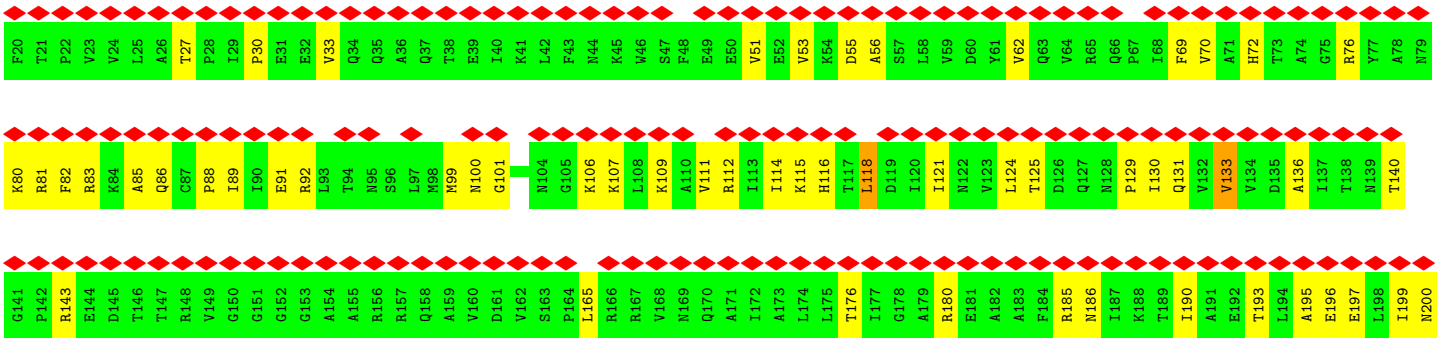


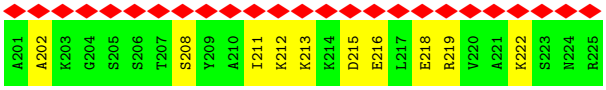


• Molecule 47: Small ribosomal subunit protein uS7

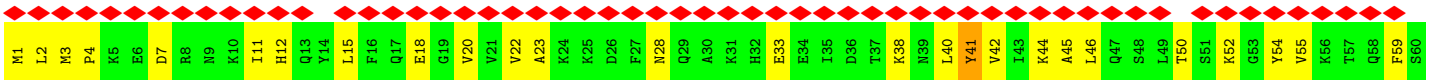
Chain SB:



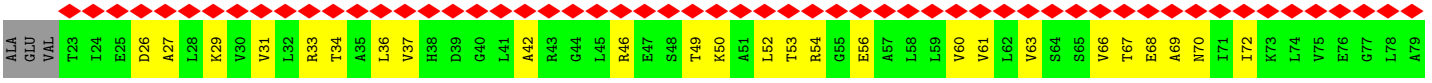


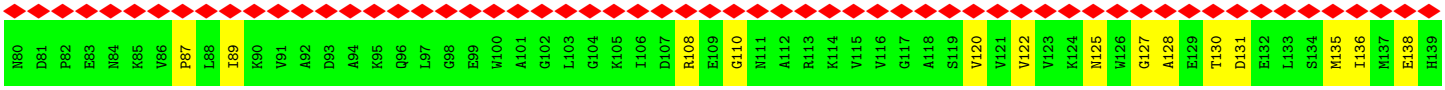


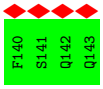
• Molecule 48: Small ribosomal subunit protein eS10A



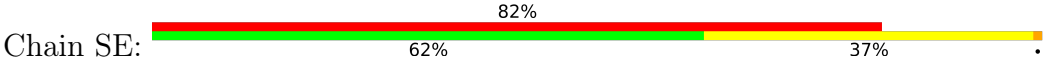
• Molecule 49: Small ribosomal subunit protein eS12

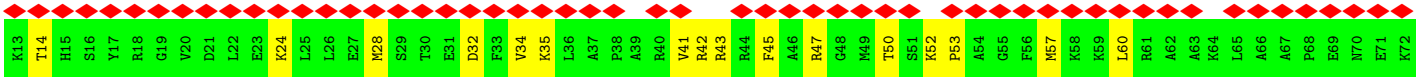


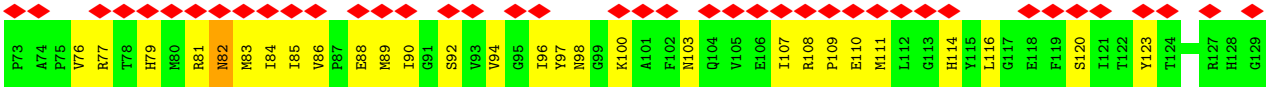




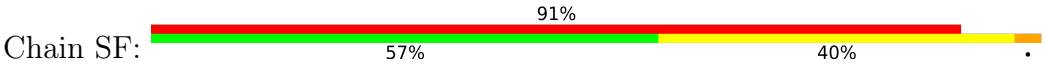
• Molecule 50: Small ribosomal subunit protein uS19

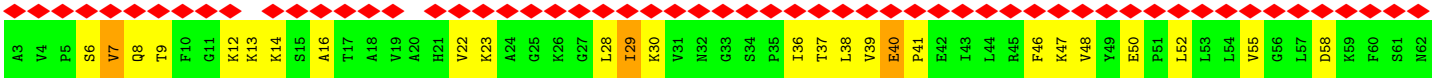


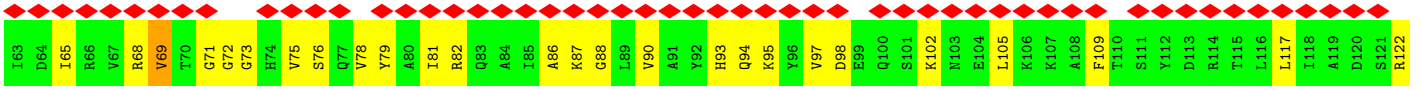


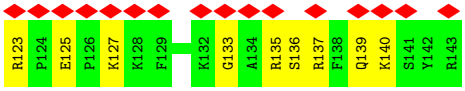


• Molecule 51: Small ribosomal subunit protein uS9A



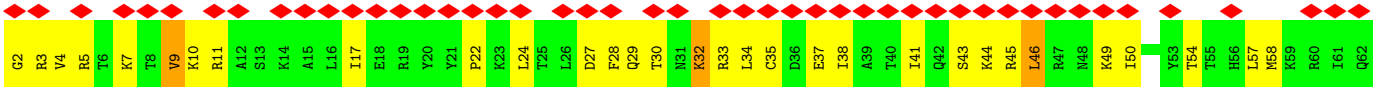


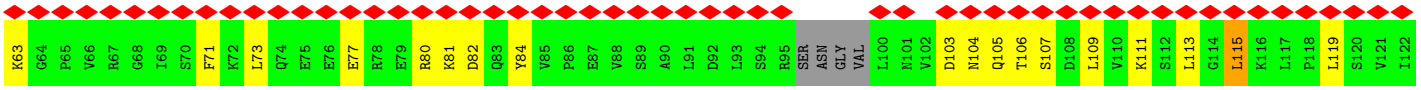


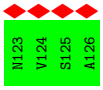


• Molecule 52: Small ribosomal subunit protein eS17A

Chain SG:

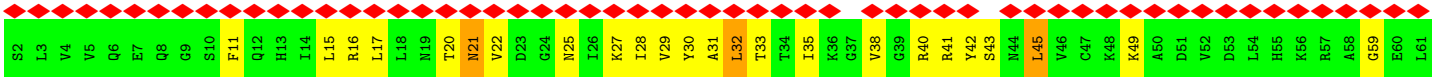


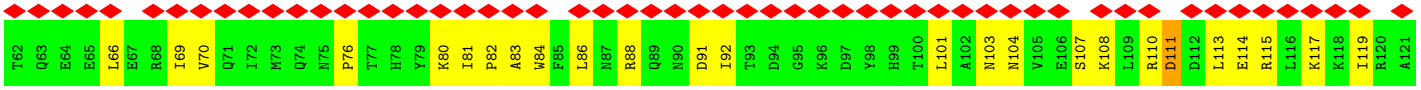


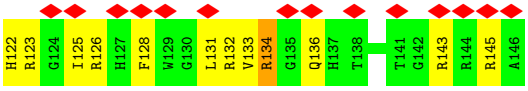


• Molecule 53: Small ribosomal subunit protein uS13A

Chain SH:

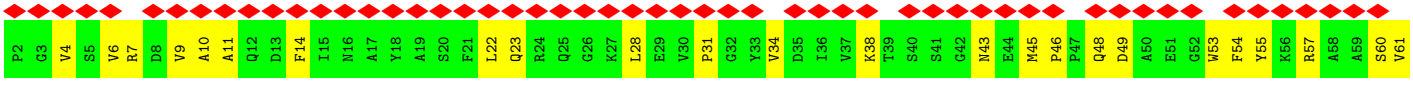


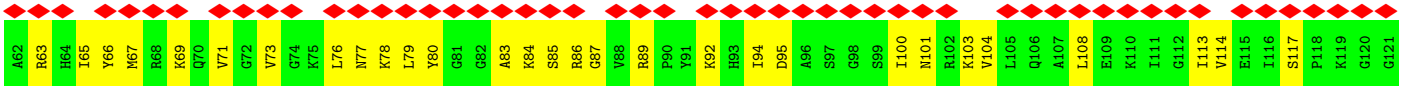


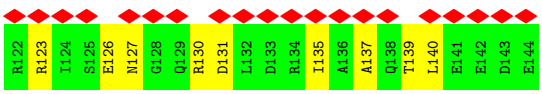


• Molecule 54: Small ribosomal subunit protein eS19A

Chain SI:

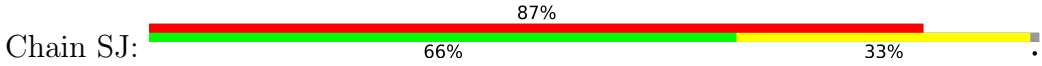


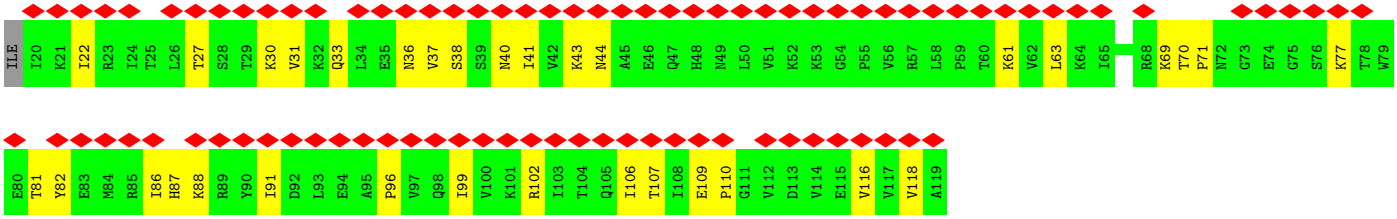




• Molecule 55: Small ribosomal subunit protein uS10

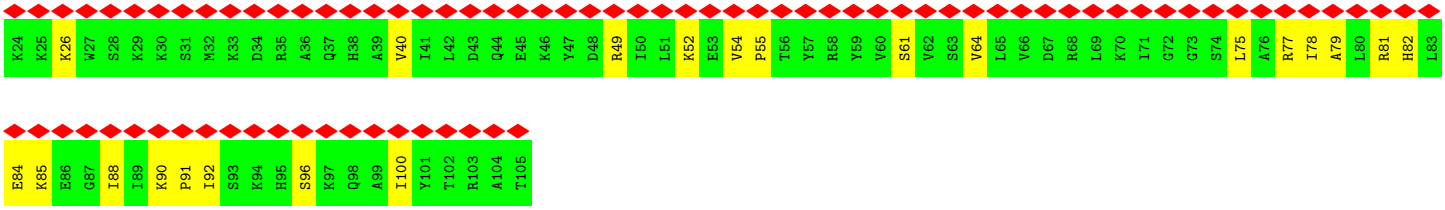
Chain SJ:





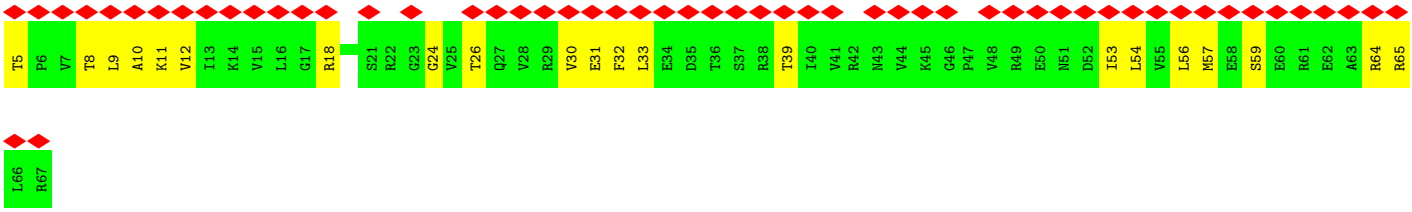
• Molecule 56: Small ribosomal subunit protein eS25A

Chain SK:



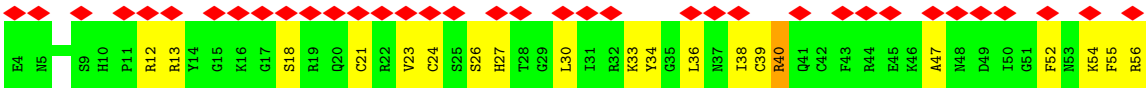
• Molecule 57: Small ribosomal subunit protein eS28A

Chain SL:



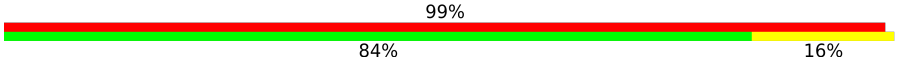
• Molecule 58: Small ribosomal subunit protein uS14A

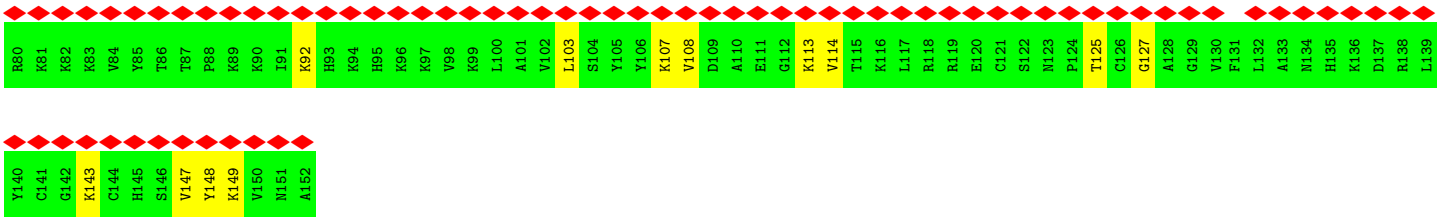
Chain SM:



• Molecule 59: Small ribosomal subunit protein eS31

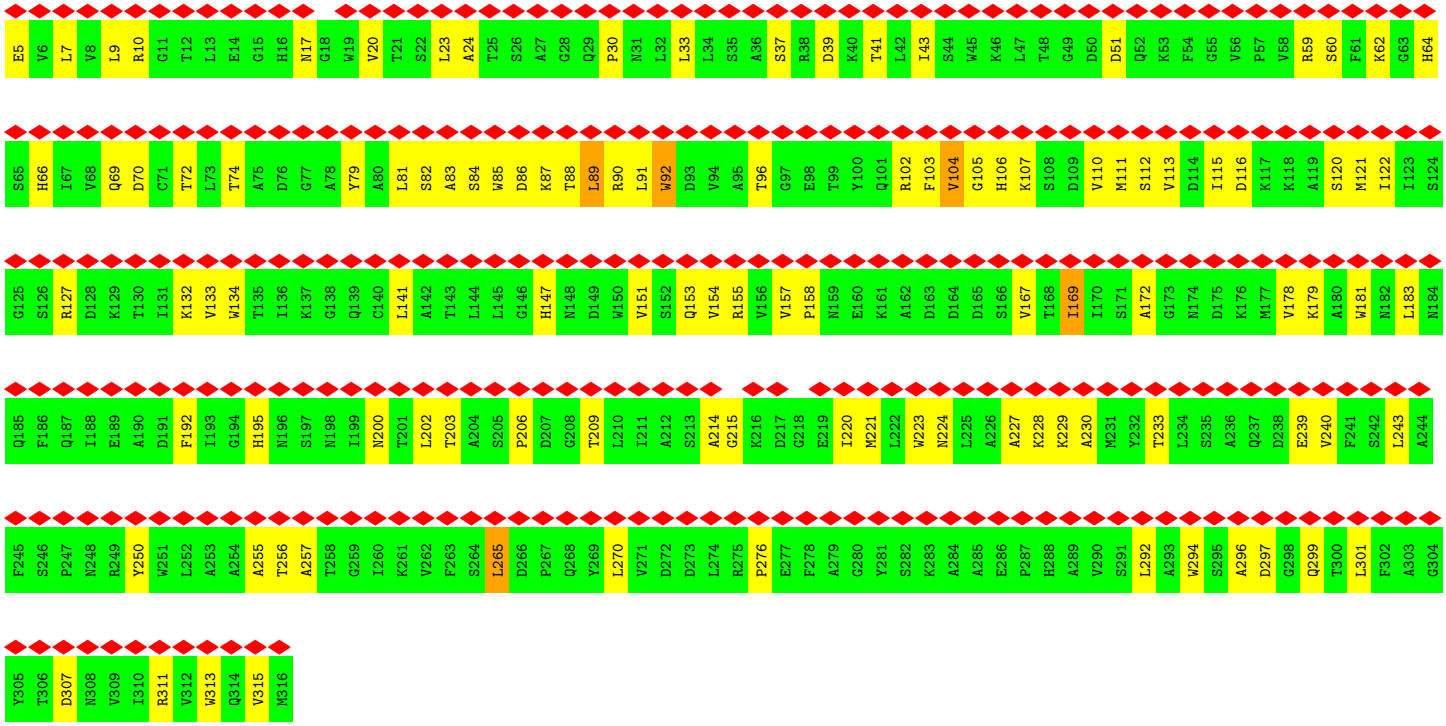
Chain SN:





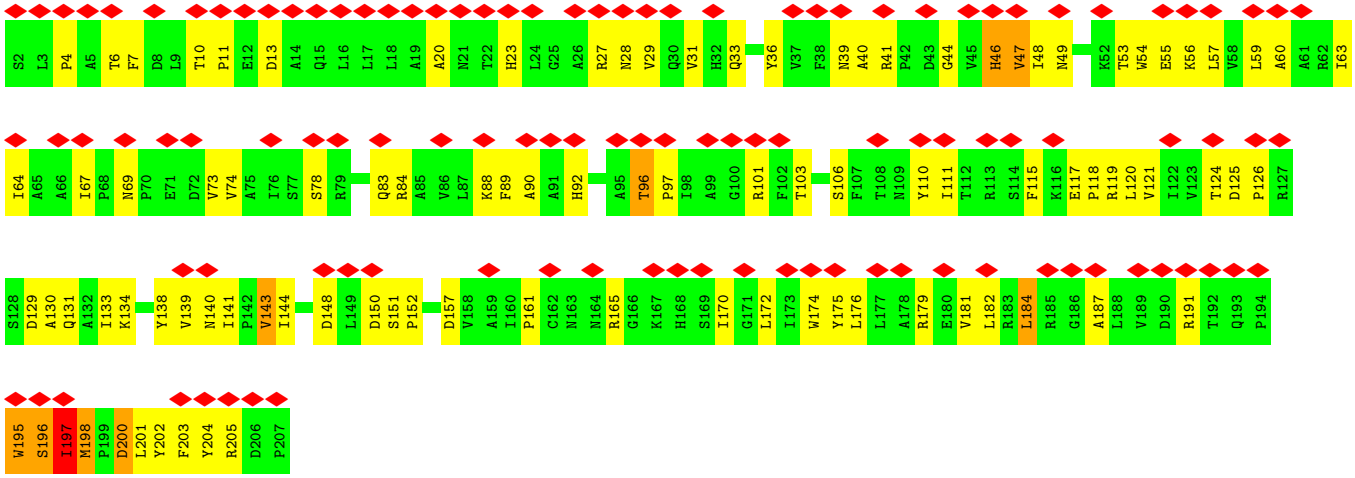
• Molecule 60: Small ribosomal subunit protein RACK1

Chain SO:



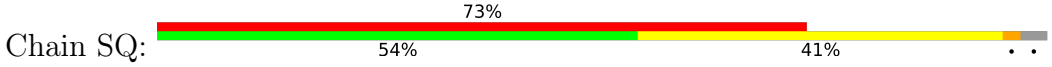
• Molecule 61: Small ribosomal subunit protein uS2A

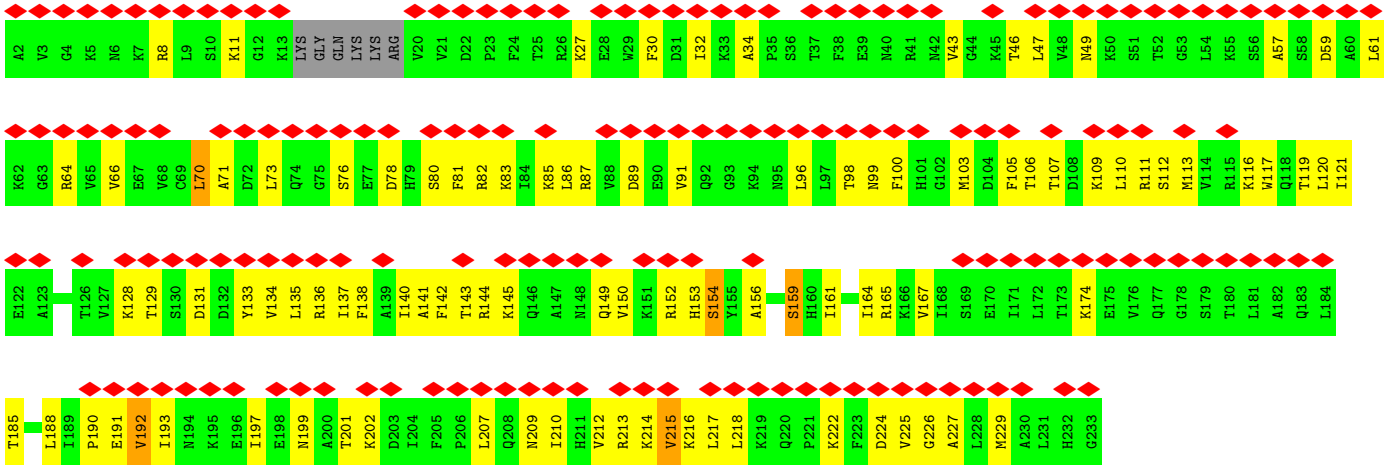
Chain SP:



• Molecule 62: Small ribosomal subunit protein eS1A

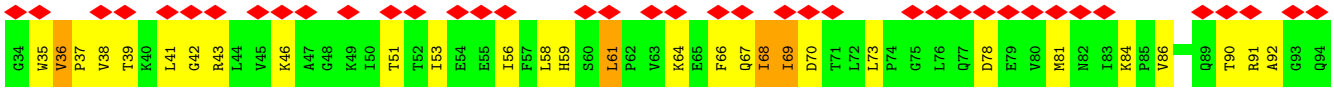
Chain SQ:

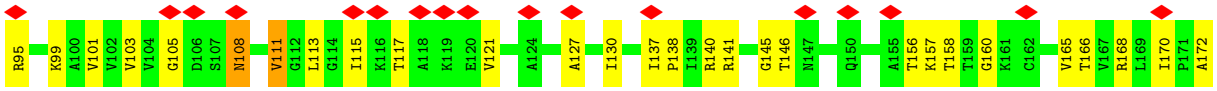


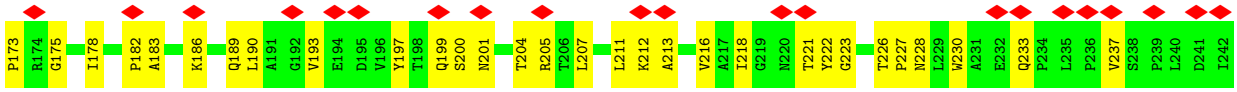


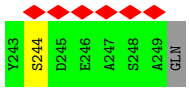
• Molecule 63: Small ribosomal subunit protein uS5

Chain SR:



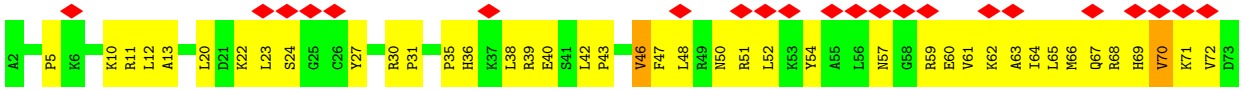


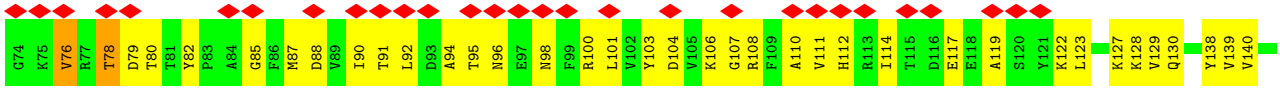


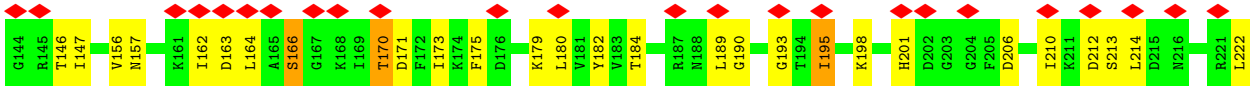


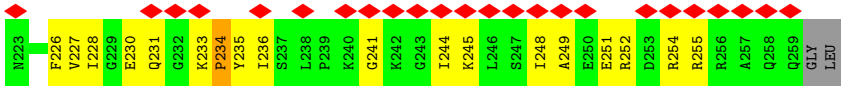
• Molecule 64: Small ribosomal subunit protein eS4A

Chain SS:



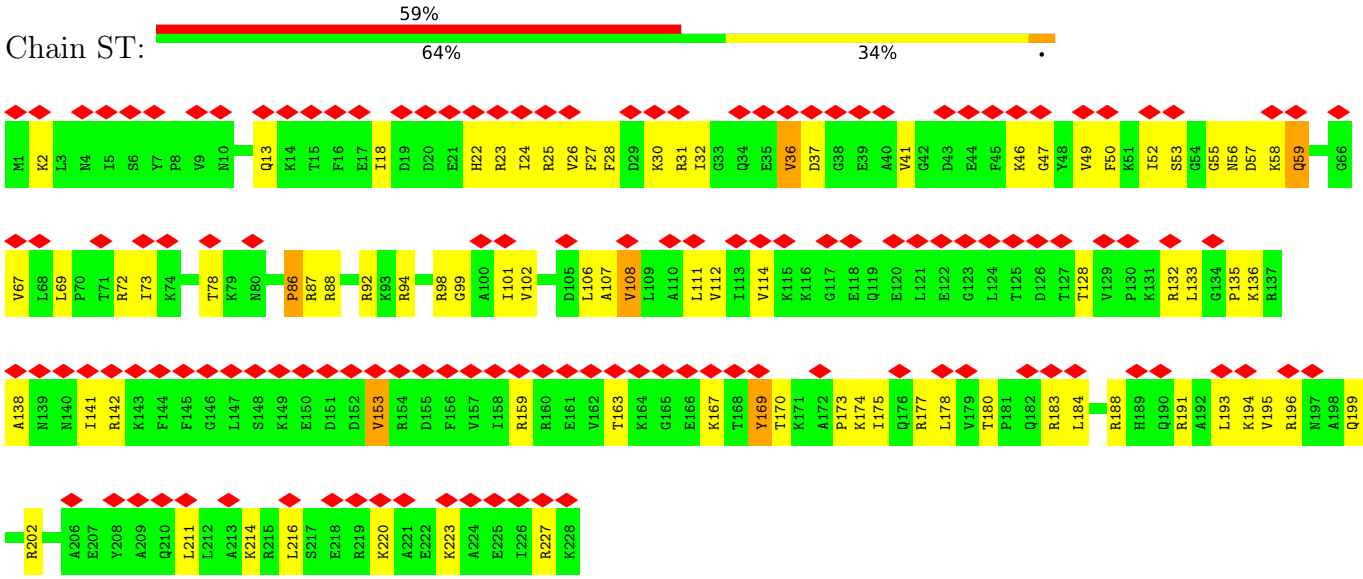






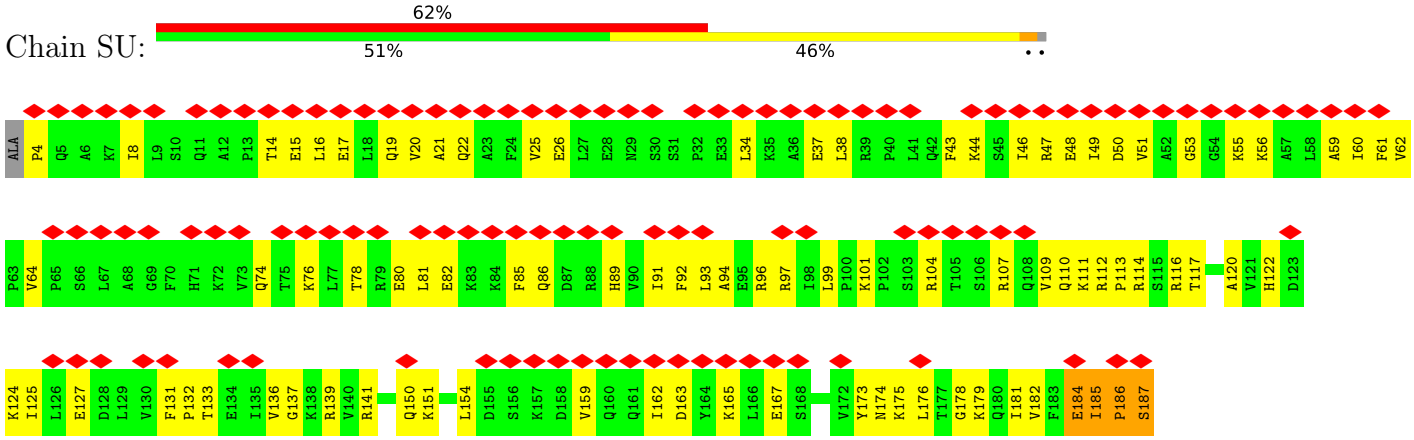
• Molecule 65: Small ribosomal subunit protein eS6A

Chain ST:



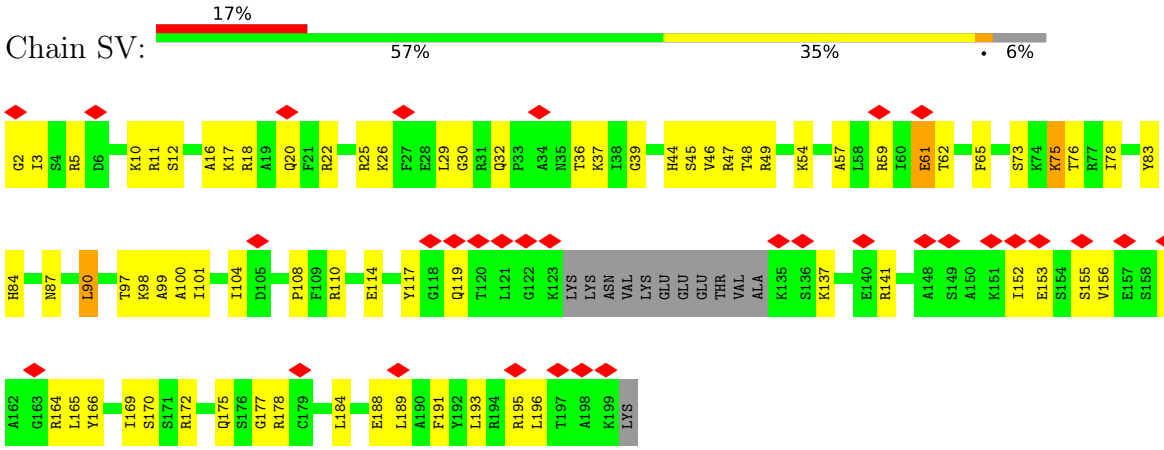
• Molecule 66: Small ribosomal subunit protein eS7A

Chain SU:



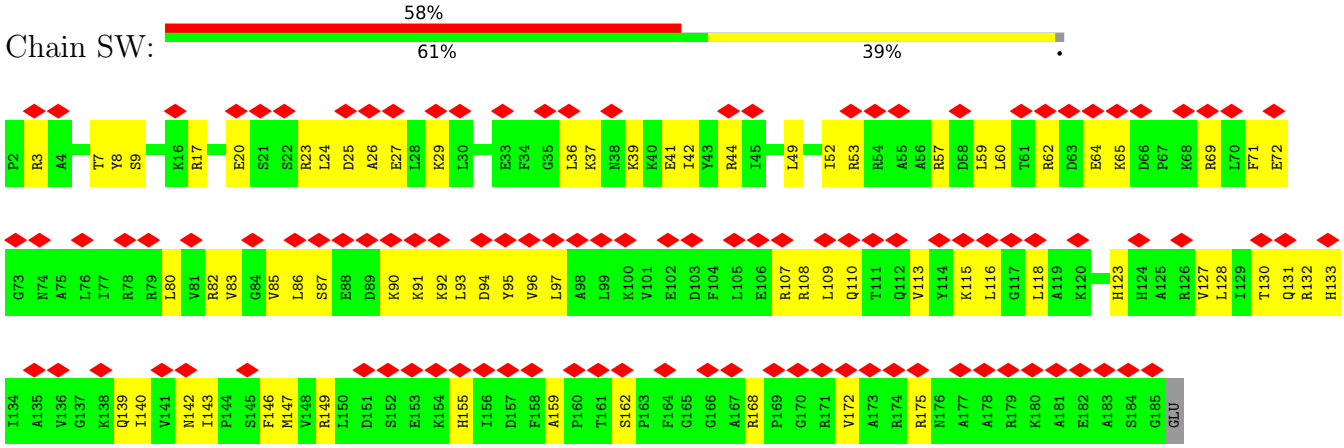
• Molecule 67: Small ribosomal subunit protein eS8A

Chain SV:



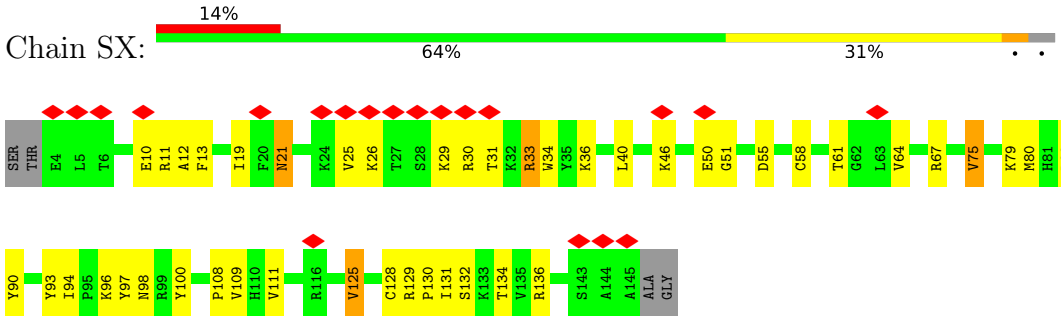
• Molecule 68: Small ribosomal subunit protein uS4A

Chain SW:



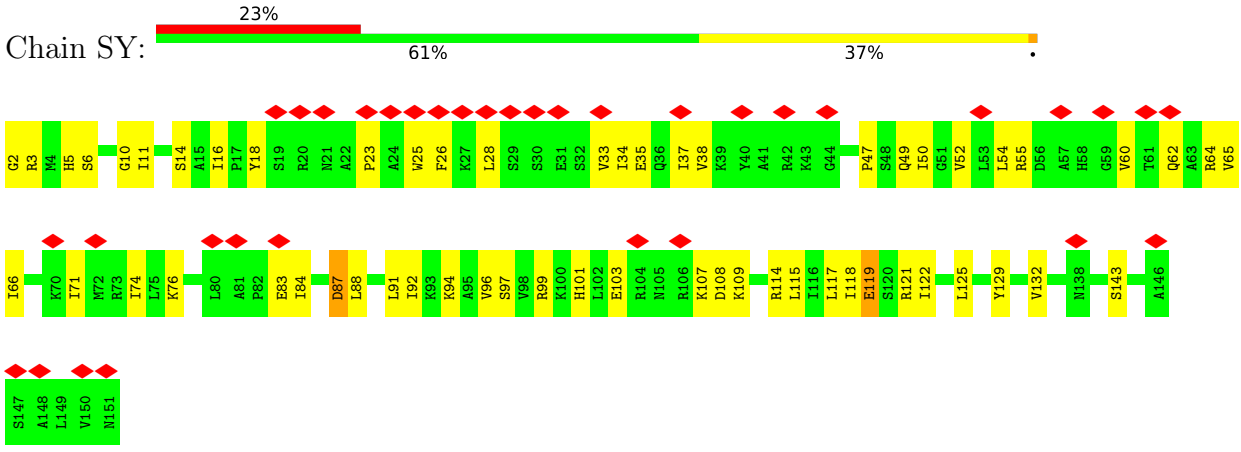
• Molecule 69: Small ribosomal subunit protein uS17A

Chain SX:



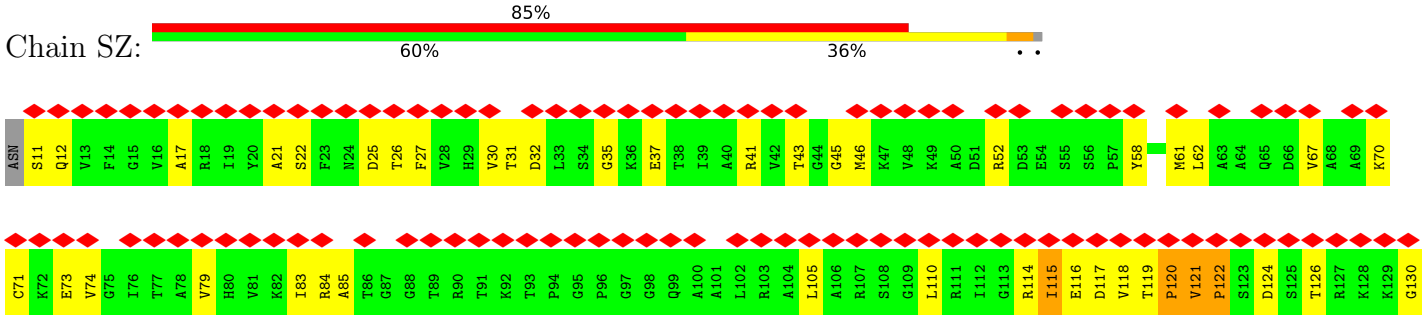
• Molecule 70: Small ribosomal subunit protein uS15

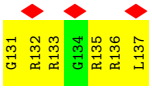
Chain SY:



• Molecule 71: Small ribosomal subunit protein uS11B

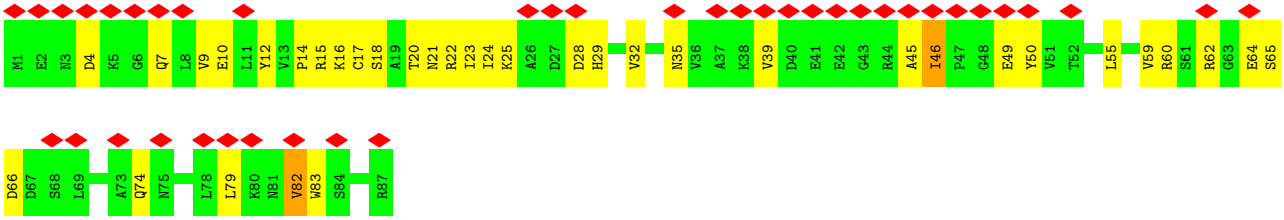
Chain SZ:





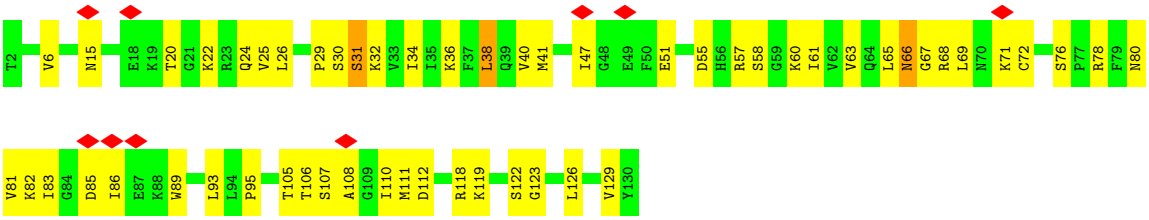
• Molecule 72: Small ribosomal subunit protein eS21A

Chain Sa:



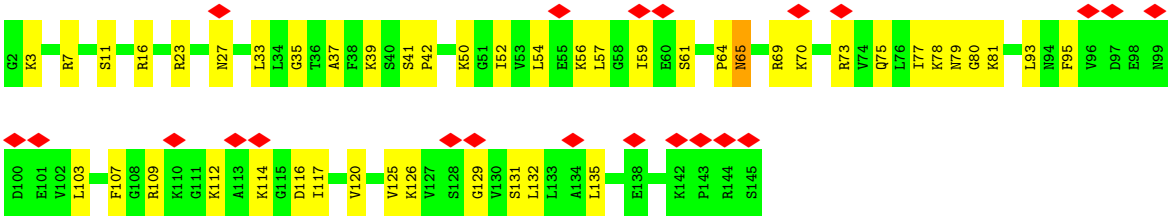
• Molecule 73: Small ribosomal subunit protein uS8A

Chain Sb:



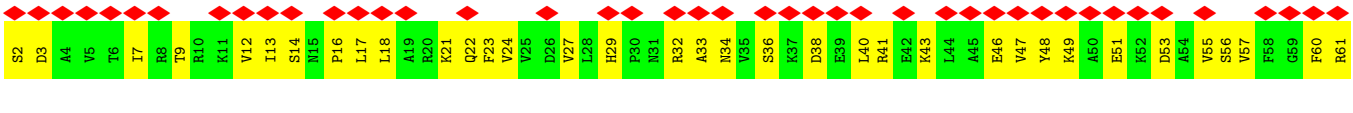
• Molecule 74: Small ribosomal subunit protein uS12A

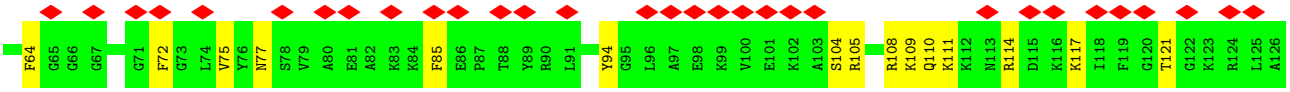
Chain Sc:

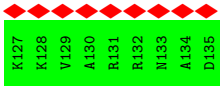


• Molecule 75: Small ribosomal subunit protein eS24A

Chain Sd:

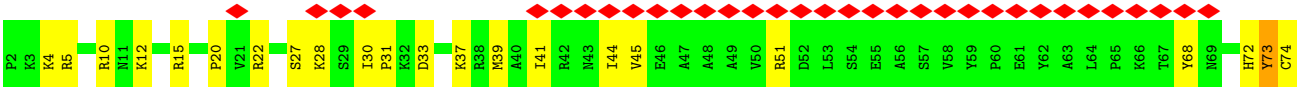


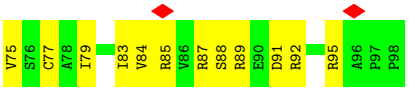




• Molecule 76: Small ribosomal subunit protein eS26B

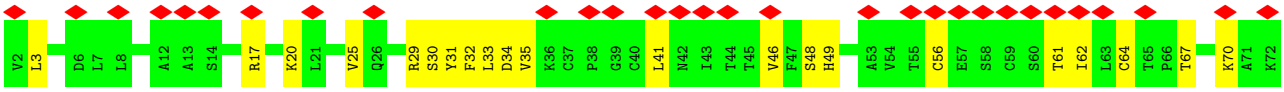
Chain Se:

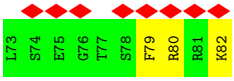




• Molecule 77: Small ribosomal subunit protein eS27A

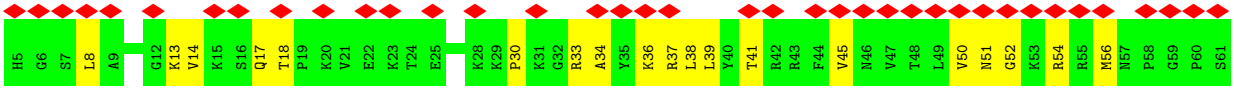
Chain Sf:





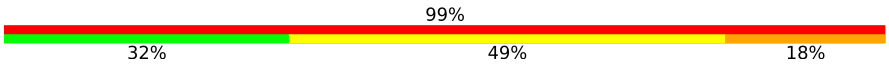
• Molecule 78: Small ribosomal subunit protein eS30A

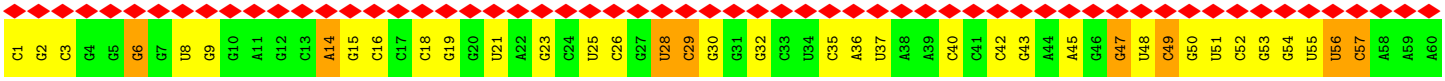
Chain Sg:

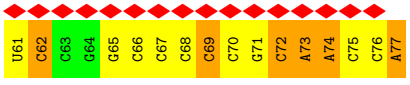


• Molecule 79: tRNA (77-MER)

Chain Ta:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80753	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.638	Depositor
Minimum map value	-1.211	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	570.0, 570.0, 570.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	LA	0.18	0/76214	0.27	0/118821
2	LB	0.15	0/2883	0.24	0/4491
3	LC	0.17	0/3746	0.26	0/5832
4	LD	0.20	0/1933	0.39	0/2598
5	LE	0.21	1/3146 (0.0%)	0.34	1/4228 (0.0%)
6	LF	0.17	0/2800	0.37	0/3790
7	LG	0.15	0/2400	0.36	0/3239
8	LH	0.16	0/1329	0.36	0/1794
9	LI	0.18	0/1821	0.33	0/2451
10	LJ	0.16	0/1836	0.36	0/2481
11	LK	0.17	0/1529	0.40	0/2060
12	LL	0.26	1/1801 (0.1%)	0.43	1/2416 (0.0%)
13	LM	0.18	0/1367	0.39	0/1834
14	LN	0.15	0/1568	0.33	0/2106
15	LO	0.16	0/1068	0.34	0/1438
16	LP	0.20	0/1757	0.36	1/2354 (0.0%)
17	LQ	0.19	0/1585	0.34	0/2128
18	LR	0.17	0/1439	0.30	0/1938
19	LS	0.17	0/1465	0.35	0/1965
20	LT	0.17	0/1532	0.32	0/2043
21	LU	0.16	0/1473	0.32	0/1980
22	LV	0.17	0/1296	0.33	0/1739
23	LW	0.16	0/812	0.38	0/1099
24	LX	0.15	0/1018	0.29	0/1369
25	LY	0.15	0/540	0.32	0/717
26	LZ	0.15	0/979	0.34	0/1321
27	La	0.14	0/995	0.34	0/1329
28	Lb	0.17	0/1106	0.38	0/1485
29	Lc	0.23	0/1200	0.49	2/1607 (0.1%)
30	Ld	0.17	0/473	0.49	1/629 (0.2%)
31	Le	0.16	0/745	0.32	0/1001
32	Lf	0.15	0/890	0.32	0/1196
33	Lg	0.15	0/1038	0.31	0/1390
34	Lh	0.18	0/868	0.36	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	Li	0.18	0/890	0.37	0/1189
36	Lj	0.16	0/978	0.32	0/1301
37	Lk	0.15	0/772	0.36	0/1026
38	Ll	0.19	0/660	0.34	0/875
39	Lm	0.46	1/618 (0.2%)	0.57	1/826 (0.1%)
40	Ln	0.16	0/443	0.28	0/588
41	Lo	0.15	0/416	0.32	0/553
42	Lp	0.12	0/230	0.23	0/296
43	Lq	0.48	0/836	0.49	0/1104
44	Lr	0.18	0/701	0.36	0/934
45	S2	0.13	0/42211	0.27	1/65773 (0.0%)
46	SA	0.30	1/1754 (0.1%)	0.62	1/2361 (0.0%)
47	SB	0.14	0/1625	0.35	0/2197
48	SC	0.22	0/769	0.34	0/1039
49	SD	0.17	0/883	0.49	0/1199
50	SE	0.15	0/936	0.35	0/1259
51	SF	0.14	0/1125	0.38	0/1510
52	SG	0.14	0/957	0.44	0/1283
53	SH	0.12	0/1207	0.32	0/1623
54	SI	0.14	0/1130	0.37	0/1517
55	SJ	0.14	0/807	0.33	0/1091
56	SK	0.11	0/661	0.34	0/888
57	SL	0.11	0/493	0.29	0/663
58	SM	0.11	0/452	0.27	0/600
59	SN	0.09	0/567	0.30	0/764
60	SO	0.13	0/2436	0.36	0/3318
61	SP	0.33	0/1644	0.62	5/2249 (0.2%)
62	SQ	0.15	0/1823	0.38	0/2447
63	SR	0.18	0/1656	0.45	0/2251
64	SS	0.39	4/2097 (0.2%)	0.58	2/2823 (0.1%)
65	ST	0.27	1/1839 (0.1%)	0.61	5/2460 (0.2%)
66	SU	0.32	0/1498	0.56	3/2019 (0.1%)
67	SV	0.37	2/1501 (0.1%)	0.55	2/2006 (0.1%)
68	SW	0.14	0/1504	0.35	0/2016
69	SX	0.15	0/1168	0.36	0/1575
70	SY	0.24	1/1215 (0.1%)	0.38	0/1638
71	SZ	0.21	0/934	0.84	5/1257 (0.4%)
72	Sa	0.18	0/682	0.48	0/921
73	Sb	0.19	0/1038	0.38	0/1395
74	Sc	0.15	0/1139	0.36	0/1518
75	Sd	0.13	0/1046	0.34	0/1401
76	Se	0.14	0/778	0.34	0/1042
77	Sf	0.14	0/620	0.31	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	Sg	0.15	0/459	0.36	0/611
79	Ta	0.18	0/1836	0.34	0/2859
All	All	0.18	12/215686 (0.0%)	0.33	31/317140 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
10	LJ	0	2
30	Ld	0	1
63	SR	0	1
71	SZ	0	4
All	All	0	8

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	SS	234	PRO	N-CD	11.04	1.63	1.47
39	Lm	70	PRO	CA-C	9.80	1.58	1.52
67	SV	108	PRO	N-CD	8.95	1.60	1.47
67	SV	108	PRO	CG-CD	-7.32	1.25	1.50
12	LL	179	PRO	N-CD	6.96	1.57	1.47

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
64	SS	234	PRO	CA-N-CD	-19.19	85.13	112.00
65	ST	86	PRO	CA-CB-CG	-15.78	74.51	104.50
67	SV	108	PRO	CA-N-CD	-14.35	91.91	112.00
46	SA	192	PRO	CA-N-CD	-14.32	91.94	112.00
65	ST	86	PRO	N-CD-CG	-12.88	83.88	103.20

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LJ	30	THR	Peptide
10	LJ	76	ALA	Peptide
30	Ld	20	GLY	Peptide

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Mol	Chain	Res	Type	Group
63	SR	233	GLN	Peptide
71	SZ	114	ARG	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	68091	0	34217	1018	0
2	LB	2579	0	1304	53	0
3	LC	3353	0	1695	67	0
4	LD	1899	0	1957	79	0
5	LE	3075	0	3142	80	0
6	LF	2748	0	2859	94	0
7	LG	2351	0	2294	83	0
8	LH	1307	0	1377	36	0
9	LI	1784	0	1862	47	0
10	LJ	1804	0	1877	53	0
11	LK	1508	0	1572	79	0
12	LL	1764	0	1804	81	0
13	LM	1346	0	1370	67	0
14	LN	1543	0	1608	49	0
15	LO	1053	0	1149	33	0
16	LP	1720	0	1779	57	0
17	LQ	1555	0	1659	45	0
18	LR	1416	0	1433	30	0
19	LS	1441	0	1543	45	0
20	LT	1515	0	1606	39	0
21	LU	1437	0	1475	38	0
22	LV	1272	0	1312	47	0
23	LW	796	0	812	20	0
24	LX	1003	0	1048	27	0
25	LY	528	0	546	14	0
26	LZ	964	0	1025	28	0
27	La	984	0	1075	32	0
28	Lb	1080	0	1122	34	0
29	Lc	1169	0	1211	42	0
30	Ld	462	0	491	18	0
31	Le	737	0	792	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Lf	876	0	912	18	0
33	Lg	1017	0	1081	29	0
34	Lh	850	0	880	25	0
35	Li	880	0	945	25	0
36	Lj	969	0	1078	27	0
37	Lk	766	0	844	21	0
38	Ll	645	0	649	20	0
39	Lm	612	0	682	24	0
40	Ln	436	0	475	12	0
41	Lo	410	0	446	11	0
42	Lp	229	0	273	8	0
43	Lq	824	0	892	19	0
44	Lr	694	0	738	22	0
45	S2	37739	0	18988	770	0
46	SA	1729	0	1812	69	0
47	SB	1605	0	1669	56	0
48	SC	752	0	719	42	0
49	SD	875	0	878	26	0
50	SE	916	0	941	37	0
51	SF	1105	0	1166	53	0
52	SG	948	0	990	42	0
53	SH	1188	0	1218	53	0
54	SI	1112	0	1124	55	0
55	SJ	797	0	863	32	0
56	SK	651	0	682	13	0
57	SL	491	0	524	16	0
58	SM	442	0	432	24	0
59	SN	556	0	549	8	0
60	SO	2383	0	2332	84	0
61	SP	1603	0	1610	72	0
62	SQ	1798	0	1890	81	0
63	SR	1626	0	1715	72	0
64	SS	2056	0	2140	106	0
65	ST	1815	0	1894	83	0
66	SU	1473	0	1555	79	0
67	SV	1476	0	1501	59	0
68	SW	1479	0	1556	65	0
69	SX	1142	0	1209	40	0
70	SY	1192	0	1255	52	0
71	SZ	923	0	948	52	0
72	Sa	673	0	662	36	0
73	Sb	1021	0	1060	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	Sc	1121	0	1196	35	0
75	Sd	1032	0	1044	48	0
76	Se	765	0	814	31	0
77	Sf	610	0	633	15	0
78	Sg	451	0	494	13	0
79	Ta	1644	0	837	25	0
All	All	200681	0	147811	4369	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 4369 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:S2:123:G:C6	45:S2:295:A:N1	1.75	1.51
1:LA:2923:U:O4	79:Ta:74:A:C2	1.67	1.45
64:SS:234:PRO:CB	64:SS:234:PRO:CG	1.74	1.39
45:S2:123:G:N1	45:S2:295:A:C2	1.94	1.36
45:S2:123:G:N1	45:S2:295:A:N1	1.71	1.34

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LD	249/251 (99%)	231 (93%)	18 (7%)	0	100	100
5	LE	384/386 (100%)	358 (93%)	26 (7%)	0	100	100
6	LF	359/361 (99%)	338 (94%)	21 (6%)	0	100	100
7	LG	292/294 (99%)	274 (94%)	18 (6%)	0	100	100
8	LH	163/175 (93%)	151 (93%)	12 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	LI	220/222 (99%)	210 (96%)	10 (4%)	0	100	100
10	LJ	231/233 (99%)	220 (95%)	11 (5%)	0	100	100
11	LK	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
12	LL	216/218 (99%)	201 (93%)	15 (7%)	0	100	100
13	LM	167/169 (99%)	158 (95%)	9 (5%)	0	100	100
14	LN	191/193 (99%)	174 (91%)	17 (9%)	0	100	100
15	LO	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
16	LP	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
17	LQ	195/197 (99%)	189 (97%)	6 (3%)	0	100	100
18	LR	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
19	LS	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
20	LT	186/188 (99%)	180 (97%)	6 (3%)	0	100	100
21	LU	169/171 (99%)	161 (95%)	8 (5%)	0	100	100
22	LV	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
23	LW	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
24	LX	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
25	LY	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
26	LZ	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
27	La	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
28	Lb	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
29	Lc	146/148 (99%)	135 (92%)	11 (8%)	0	100	100
30	Ld	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
31	Le	94/96 (98%)	94 (100%)	0	0	100	100
32	Lf	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
33	Lg	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
34	Lh	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
35	Li	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
36	Lj	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
37	Lk	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
38	Ll	79/81 (98%)	77 (98%)	2 (2%)	0	100	100
39	Lm	75/77 (97%)	75 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Ln	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
41	Lo	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	Lp	23/25 (92%)	23 (100%)	0	0	100	100
43	Lq	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
44	Lr	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
46	SA	220/223 (99%)	212 (96%)	7 (3%)	1 (0%)	25	49
47	SB	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
48	SC	90/92 (98%)	83 (92%)	7 (8%)	0	100	100
49	SD	119/124 (96%)	97 (82%)	22 (18%)	0	100	100
50	SE	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
51	SF	139/141 (99%)	129 (93%)	9 (6%)	1 (1%)	19	42
52	SG	117/125 (94%)	105 (90%)	12 (10%)	0	100	100
53	SH	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
54	SI	141/143 (99%)	130 (92%)	11 (8%)	0	100	100
55	SJ	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
56	SK	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
57	SL	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
58	SM	51/53 (96%)	51 (100%)	0	0	100	100
59	SN	71/73 (97%)	58 (82%)	13 (18%)	0	100	100
60	SO	310/312 (99%)	288 (93%)	22 (7%)	0	100	100
61	SP	204/206 (99%)	182 (89%)	21 (10%)	1 (0%)	25	49
62	SQ	222/232 (96%)	207 (93%)	15 (7%)	0	100	100
63	SR	214/217 (99%)	196 (92%)	18 (8%)	0	100	100
64	SS	256/260 (98%)	234 (91%)	22 (9%)	0	100	100
65	ST	226/228 (99%)	215 (95%)	11 (5%)	0	100	100
66	SU	182/185 (98%)	172 (94%)	9 (5%)	1 (0%)	25	49
67	SV	183/199 (92%)	169 (92%)	14 (8%)	0	100	100
68	SW	182/185 (98%)	171 (94%)	11 (6%)	0	100	100
69	SX	140/146 (96%)	133 (95%)	7 (5%)	0	100	100
70	SY	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
71	SZ	125/128 (98%)	108 (86%)	16 (13%)	1 (1%)	16	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Sa	85/87 (98%)	78 (92%)	7 (8%)	0	100	100
73	Sb	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
74	Sc	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
75	Sd	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
76	Se	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
77	Sf	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
78	Sg	55/57 (96%)	50 (91%)	5 (9%)	0	100	100
All	All	10914/11115 (98%)	10236 (94%)	673 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	SA	164	VAL
51	SF	40	GLU
66	SU	186	PRO
71	SZ	115	ILE
61	SP	197	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LD	190/193 (98%)	182 (96%)	8 (4%)	25	53
5	LE	318/322 (99%)	309 (97%)	9 (3%)	38	68
6	LF	288/288 (100%)	273 (95%)	15 (5%)	19	44
7	LG	241/243 (99%)	234 (97%)	7 (3%)	37	67
8	LH	139/154 (90%)	131 (94%)	8 (6%)	17	39
9	LI	186/186 (100%)	182 (98%)	4 (2%)	47	76
10	LJ	187/191 (98%)	181 (97%)	6 (3%)	34	63
11	LK	168/171 (98%)	154 (92%)	14 (8%)	9	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	LL	185/185 (100%)	174 (94%)	11 (6%)	16 38
13	LM	145/147 (99%)	133 (92%)	12 (8%)	9 22
14	LN	154/154 (100%)	146 (95%)	8 (5%)	19 44
15	LO	107/107 (100%)	103 (96%)	4 (4%)	29 58
16	LP	175/175 (100%)	173 (99%)	2 (1%)	70 87
17	LQ	160/160 (100%)	155 (97%)	5 (3%)	35 64
18	LR	138/145 (95%)	134 (97%)	4 (3%)	37 67
19	LS	150/150 (100%)	146 (97%)	4 (3%)	40 69
20	LT	152/153 (99%)	148 (97%)	4 (3%)	41 70
21	LU	155/155 (100%)	144 (93%)	11 (7%)	12 30
22	LV	135/136 (99%)	126 (93%)	9 (7%)	13 33
23	LW	87/87 (100%)	81 (93%)	6 (7%)	13 31
24	LX	104/104 (100%)	99 (95%)	5 (5%)	21 48
25	LY	54/57 (95%)	51 (94%)	3 (6%)	17 41
26	LZ	104/105 (99%)	98 (94%)	6 (6%)	17 39
27	La	108/108 (100%)	102 (94%)	6 (6%)	17 41
28	Lb	112/115 (97%)	107 (96%)	5 (4%)	23 50
29	Lc	117/118 (99%)	111 (95%)	6 (5%)	20 45
30	Ld	46/46 (100%)	43 (94%)	3 (6%)	14 34
31	Le	81/81 (100%)	77 (95%)	4 (5%)	21 47
32	Lf	92/96 (96%)	84 (91%)	8 (9%)	8 20
33	Lg	108/109 (99%)	103 (95%)	5 (5%)	23 49
34	Lh	90/90 (100%)	83 (92%)	7 (8%)	10 26
35	Li	95/95 (100%)	94 (99%)	1 (1%)	70 87
36	Lj	104/104 (100%)	103 (99%)	1 (1%)	73 89
37	Lk	80/81 (99%)	75 (94%)	5 (6%)	15 35
38	Ll	67/67 (100%)	65 (97%)	2 (3%)	36 65
39	Lm	68/68 (100%)	67 (98%)	1 (2%)	60 83
40	Ln	45/45 (100%)	44 (98%)	1 (2%)	47 76
41	Lo	45/47 (96%)	45 (100%)	0	100 100
42	Lp	22/23 (96%)	20 (91%)	2 (9%)	7 19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	Lq	87/88 (99%)	85 (98%)	2 (2%)	45	74
44	Lr	71/71 (100%)	69 (97%)	2 (3%)	38	68
46	SA	182/182 (100%)	172 (94%)	10 (6%)	18	41
47	SB	172/173 (99%)	168 (98%)	4 (2%)	45	74
48	SC	77/85 (91%)	75 (97%)	2 (3%)	41	70
49	SD	88/100 (88%)	87 (99%)	1 (1%)	70	87
50	SE	95/98 (97%)	92 (97%)	3 (3%)	34	63
51	SF	117/117 (100%)	114 (97%)	3 (3%)	41	70
52	SG	101/113 (89%)	95 (94%)	6 (6%)	16	38
53	SH	127/128 (99%)	118 (93%)	9 (7%)	12	30
54	SI	115/115 (100%)	112 (97%)	3 (3%)	41	70
55	SJ	93/94 (99%)	92 (99%)	1 (1%)	70	87
56	SK	67/73 (92%)	65 (97%)	2 (3%)	36	65
57	SL	55/56 (98%)	52 (94%)	3 (6%)	18	41
58	SM	47/47 (100%)	46 (98%)	1 (2%)	48	76
59	SN	56/64 (88%)	56 (100%)	0	100	100
60	SO	250/257 (97%)	240 (96%)	10 (4%)	27	55
61	SP	170/173 (98%)	157 (92%)	13 (8%)	11	27
62	SQ	200/205 (98%)	190 (95%)	10 (5%)	20	46
63	SR	175/176 (99%)	162 (93%)	13 (7%)	11	28
64	SS	220/221 (100%)	206 (94%)	14 (6%)	14	34
65	ST	189/195 (97%)	181 (96%)	8 (4%)	25	53
66	SU	163/165 (99%)	152 (93%)	11 (7%)	13	33
67	SV	148/160 (92%)	140 (95%)	8 (5%)	18	42
68	SW	156/158 (99%)	154 (99%)	2 (1%)	65	85
69	SX	126/129 (98%)	120 (95%)	6 (5%)	21	48
70	SY	127/127 (100%)	122 (96%)	5 (4%)	27	56
71	SZ	90/97 (93%)	89 (99%)	1 (1%)	70	87
72	Sa	71/74 (96%)	67 (94%)	4 (6%)	17	41
73	Sb	110/110 (100%)	106 (96%)	4 (4%)	30	59
74	Sc	119/119 (100%)	114 (96%)	5 (4%)	25	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
75	Sd	102/112 (91%)	101 (99%)	1 (1%)	73 89
76	Se	82/83 (99%)	81 (99%)	1 (1%)	67 86
77	Sf	70/70 (100%)	69 (99%)	1 (1%)	62 84
78	Sg	48/49 (98%)	45 (94%)	3 (6%)	15 35
All	All	9168/9345 (98%)	8774 (96%)	394 (4%)	27 52

5 of 394 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	SA	160	SER
61	SP	39	ASN
47	SB	165	LEU
53	SH	103	ASN
62	SQ	129	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
60	SO	184	ASN
65	ST	139	ASN
61	SP	46	HIS
62	SQ	183	GLN
66	SU	122	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3181/3393 (93%)	752 (23%)	33 (1%)
2	LB	120/121 (99%)	24 (20%)	1 (0%)
3	LC	157/158 (99%)	43 (27%)	3 (1%)
45	S2	1768/1800 (98%)	764 (43%)	29 (1%)
79	Ta	76/77 (98%)	44 (57%)	0
All	All	5302/5549 (95%)	1627 (30%)	66 (1%)

5 of 1627 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	4	U

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Mol	Chain	Res	Type
1	LA	6	A
1	LA	13	A
1	LA	14	U
1	LA	25	U

5 of 66 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	S2	1252	C
45	S2	1421	A
45	S2	1688	U
1	LA	2524	G
1	LA	2502	G

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

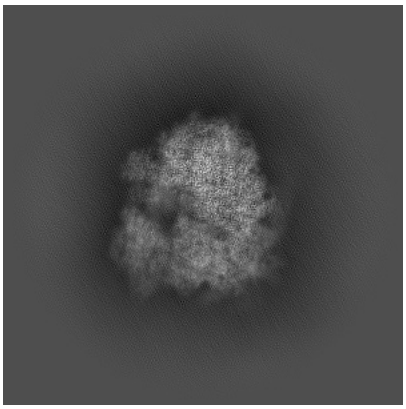
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60088. These allow visual inspection of the internal detail of the map and identification of artifacts.

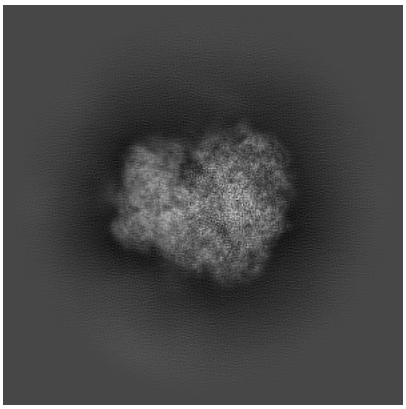
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

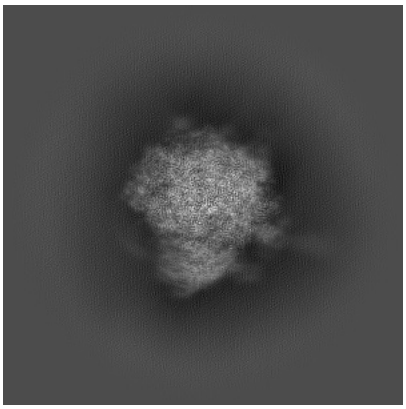
6.1.1 Primary map



X

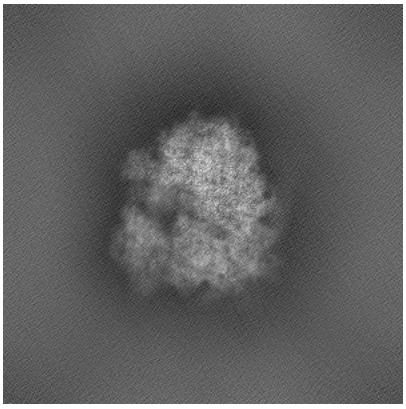


Y

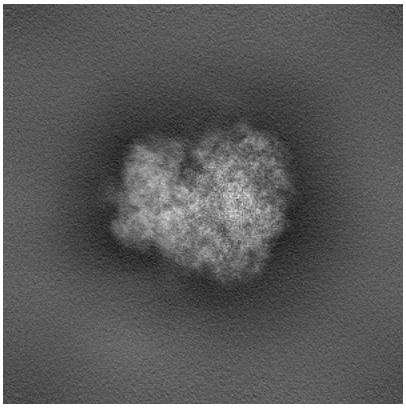


Z

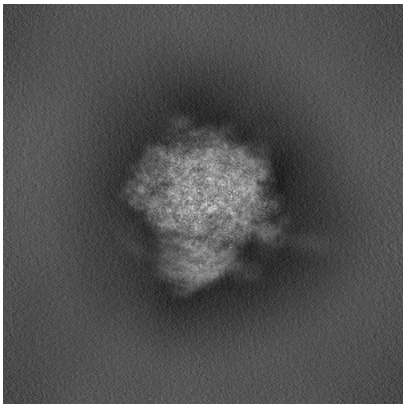
6.1.2 Raw map



X



Y

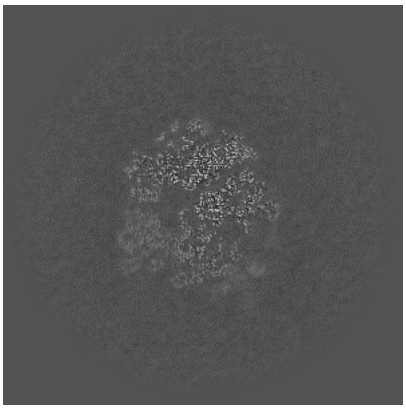


Z

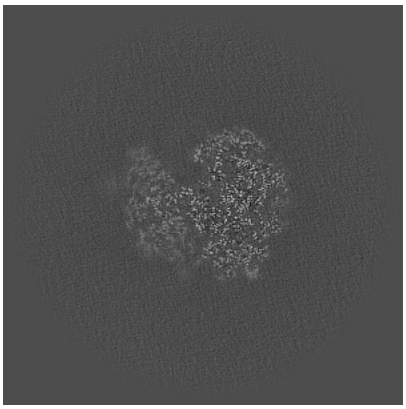
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

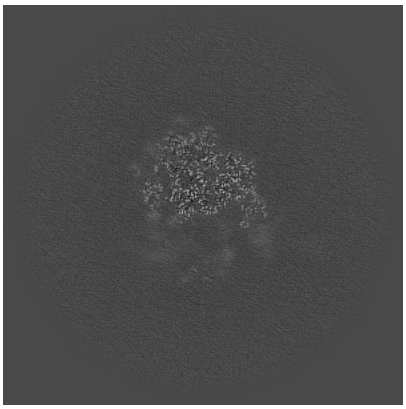
6.2.1 Primary map



X Index: 300

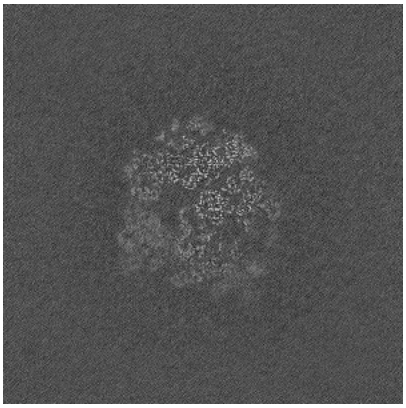


Y Index: 300

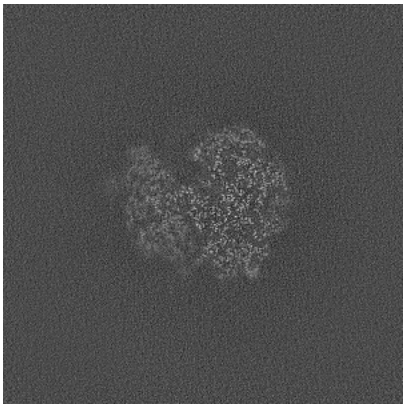


Z Index: 300

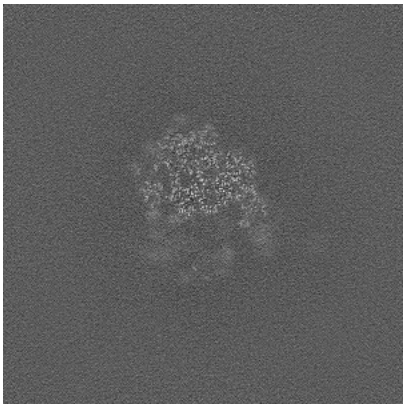
6.2.2 Raw map



X Index: 300



Y Index: 300

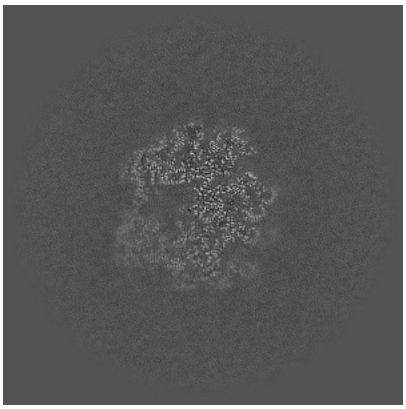


Z Index: 300

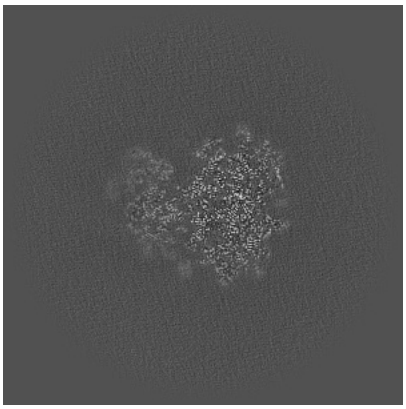
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

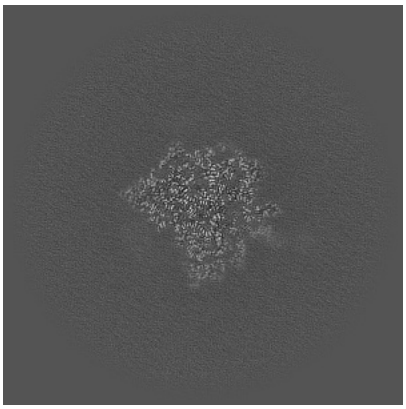
6.3.1 Primary map



X Index: 288

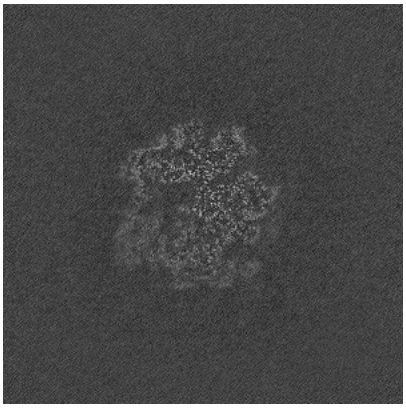


Y Index: 307

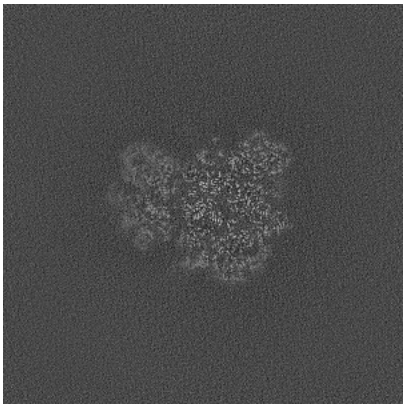


Z Index: 341

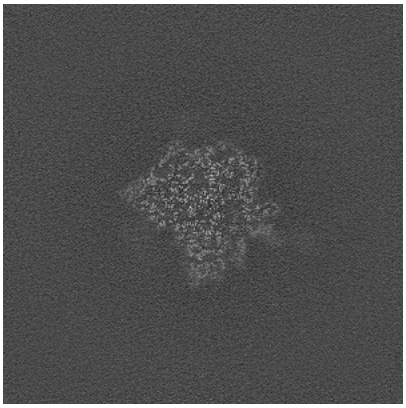
6.3.2 Raw map



X Index: 289



Y Index: 319

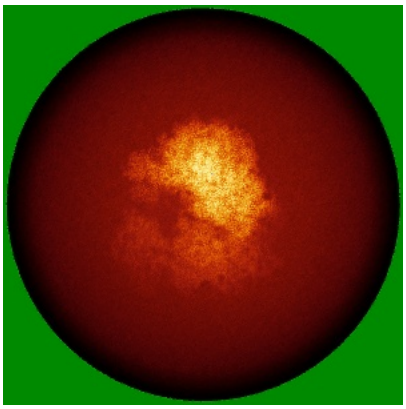


Z Index: 341

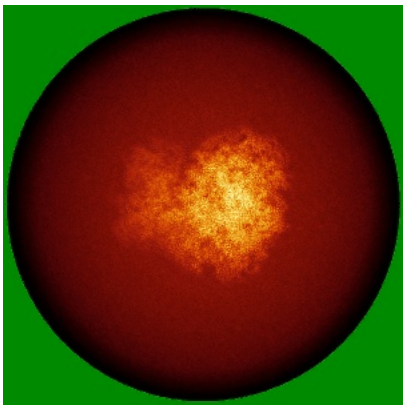
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

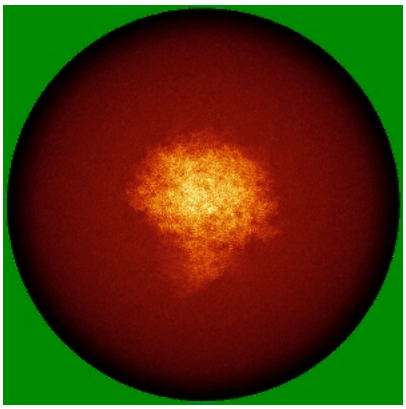
6.4.1 Primary map



X

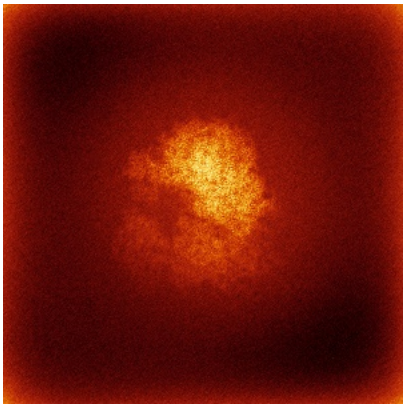


Y

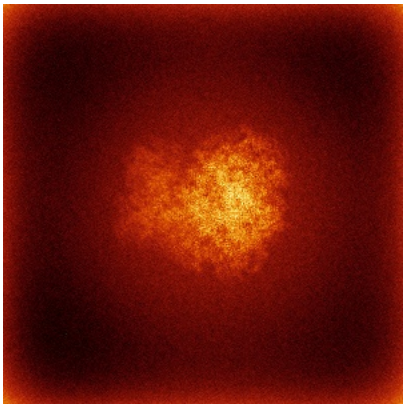


Z

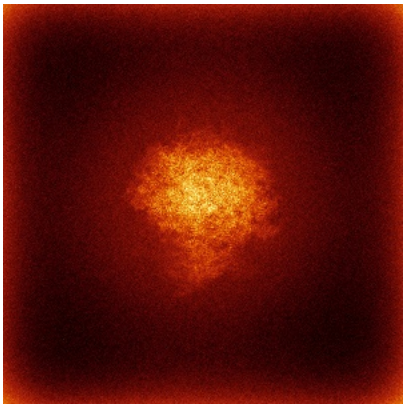
6.4.2 Raw map



X



Y

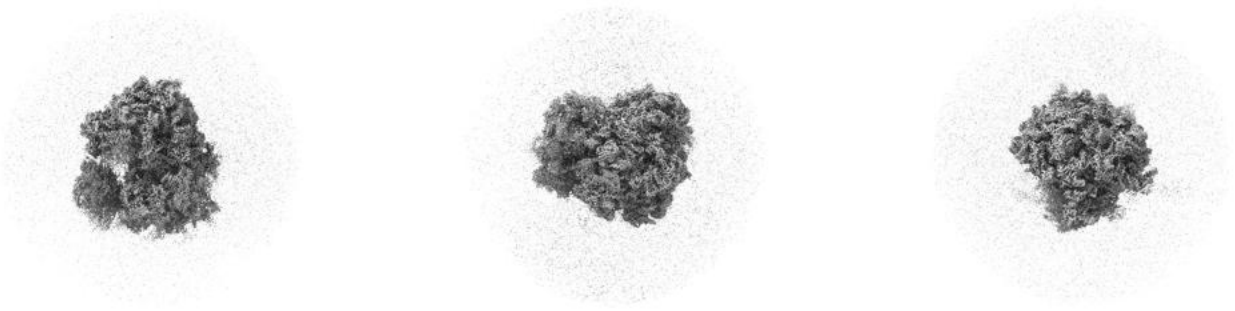


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

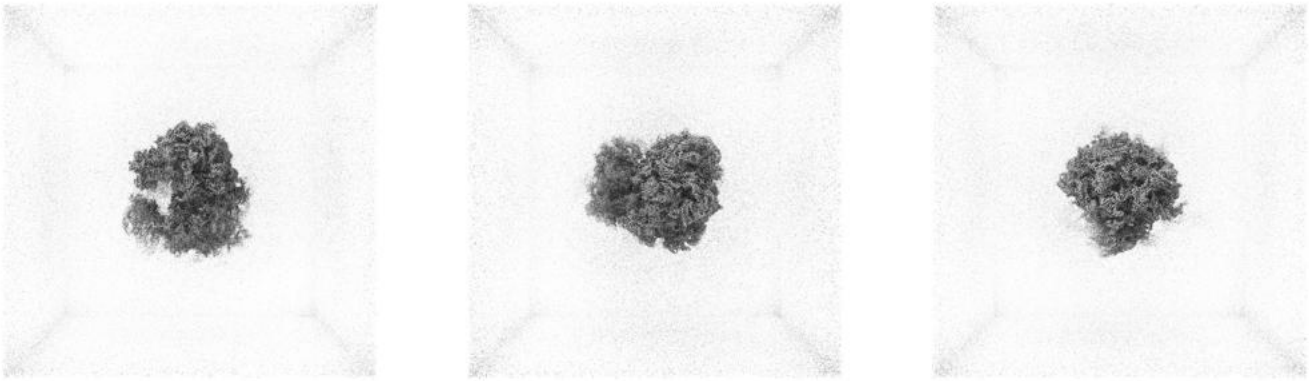
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

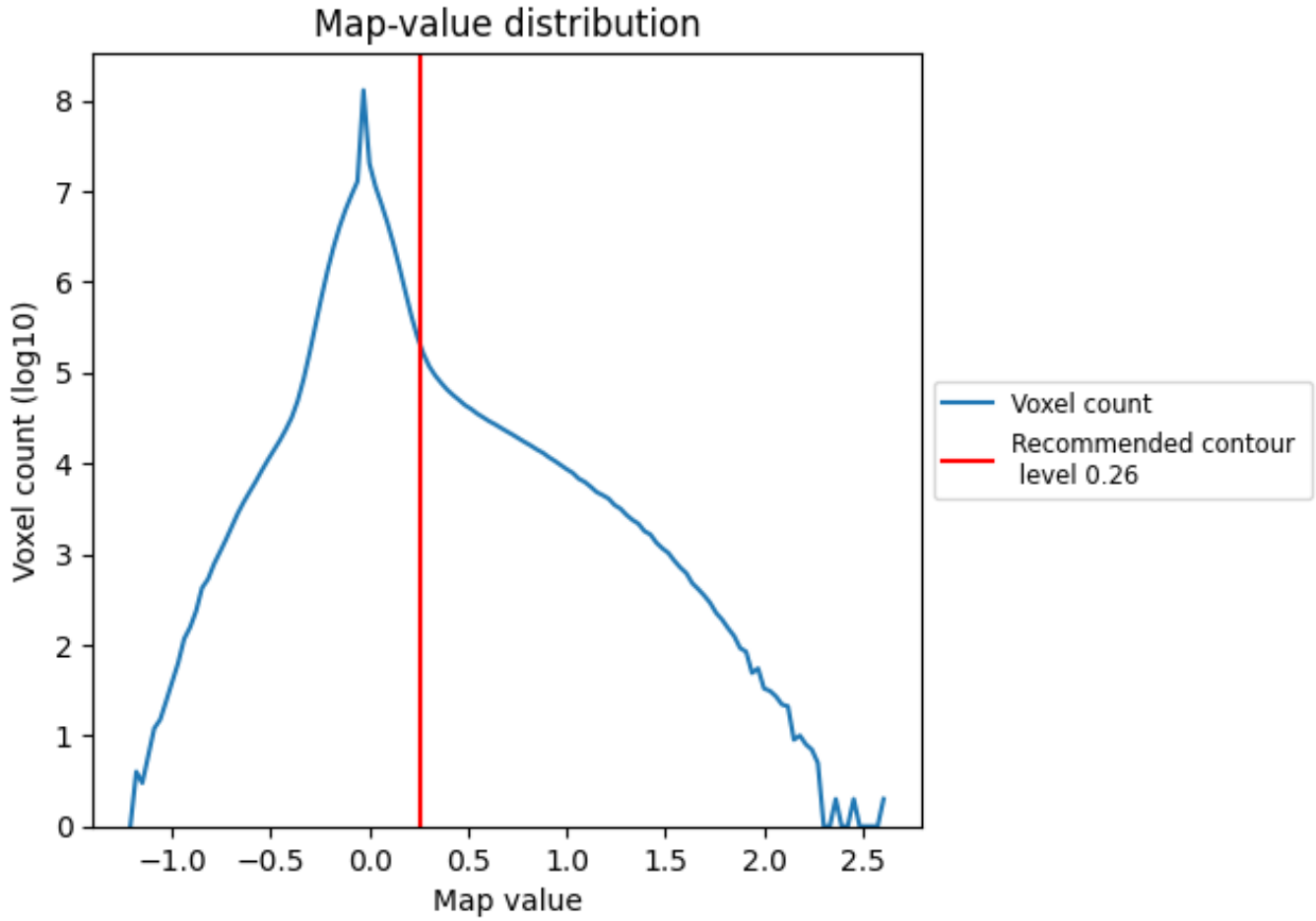
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

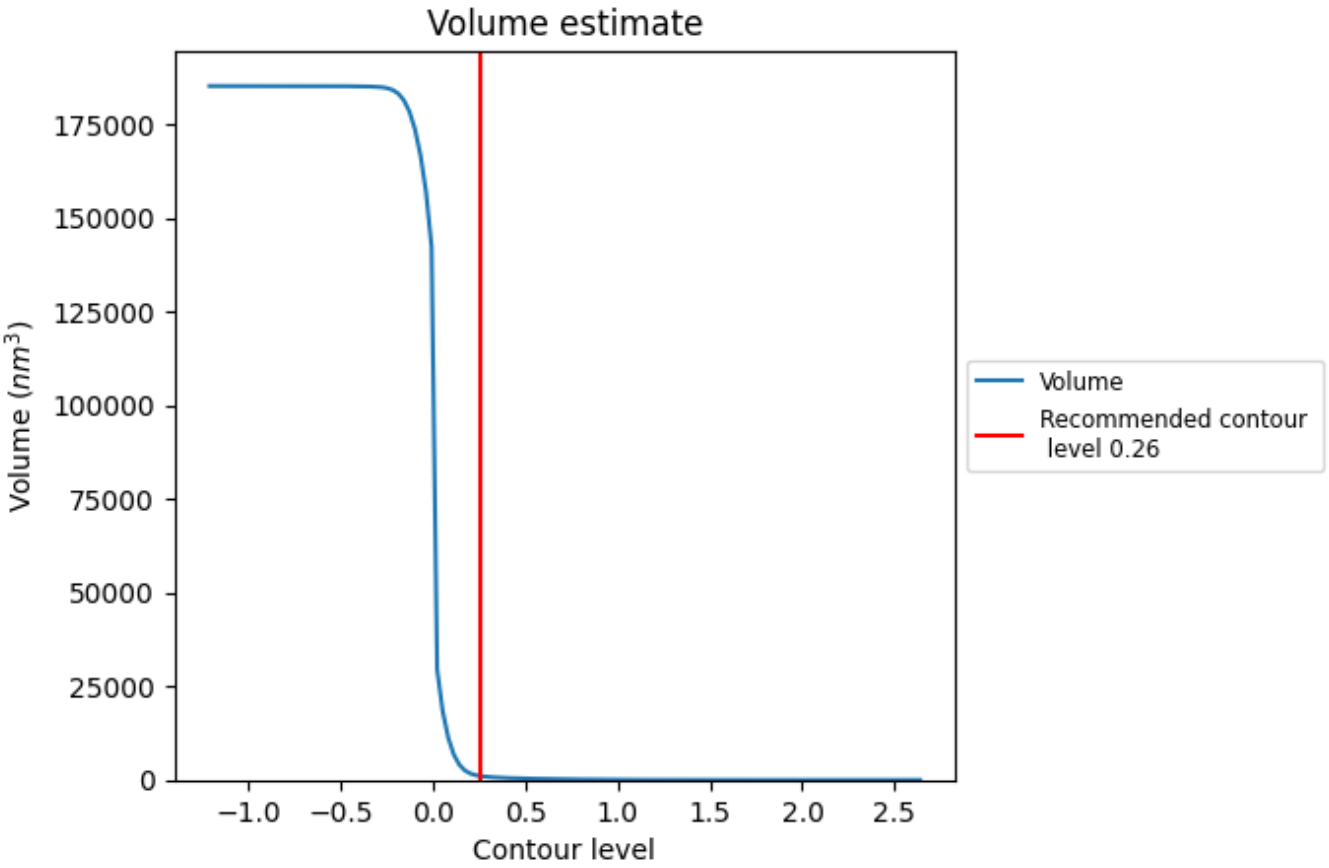
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

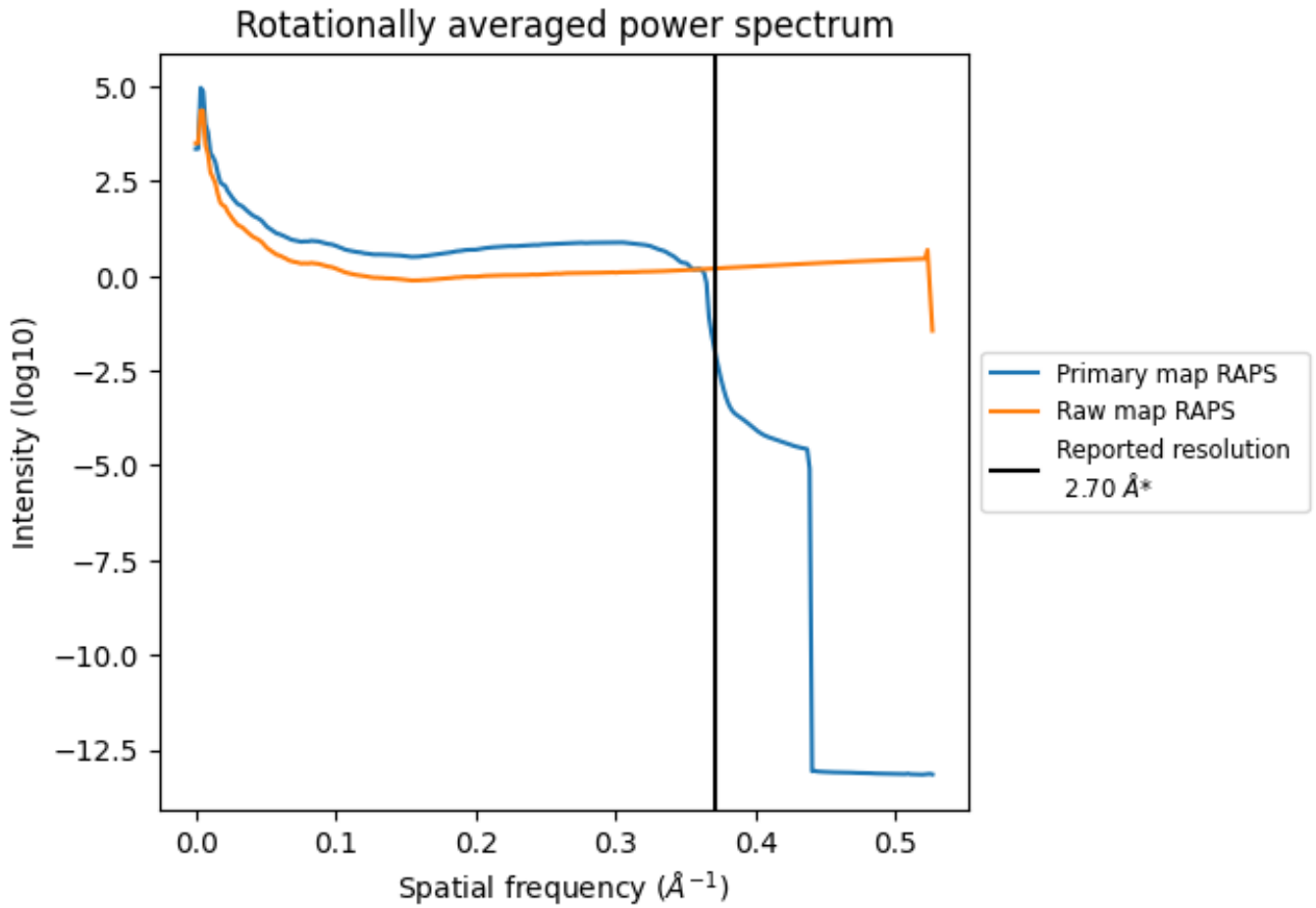
7.2 Volume estimate (i)



The volume at the recommended contour level is 1015 nm^3; this corresponds to an approximate mass of 917 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

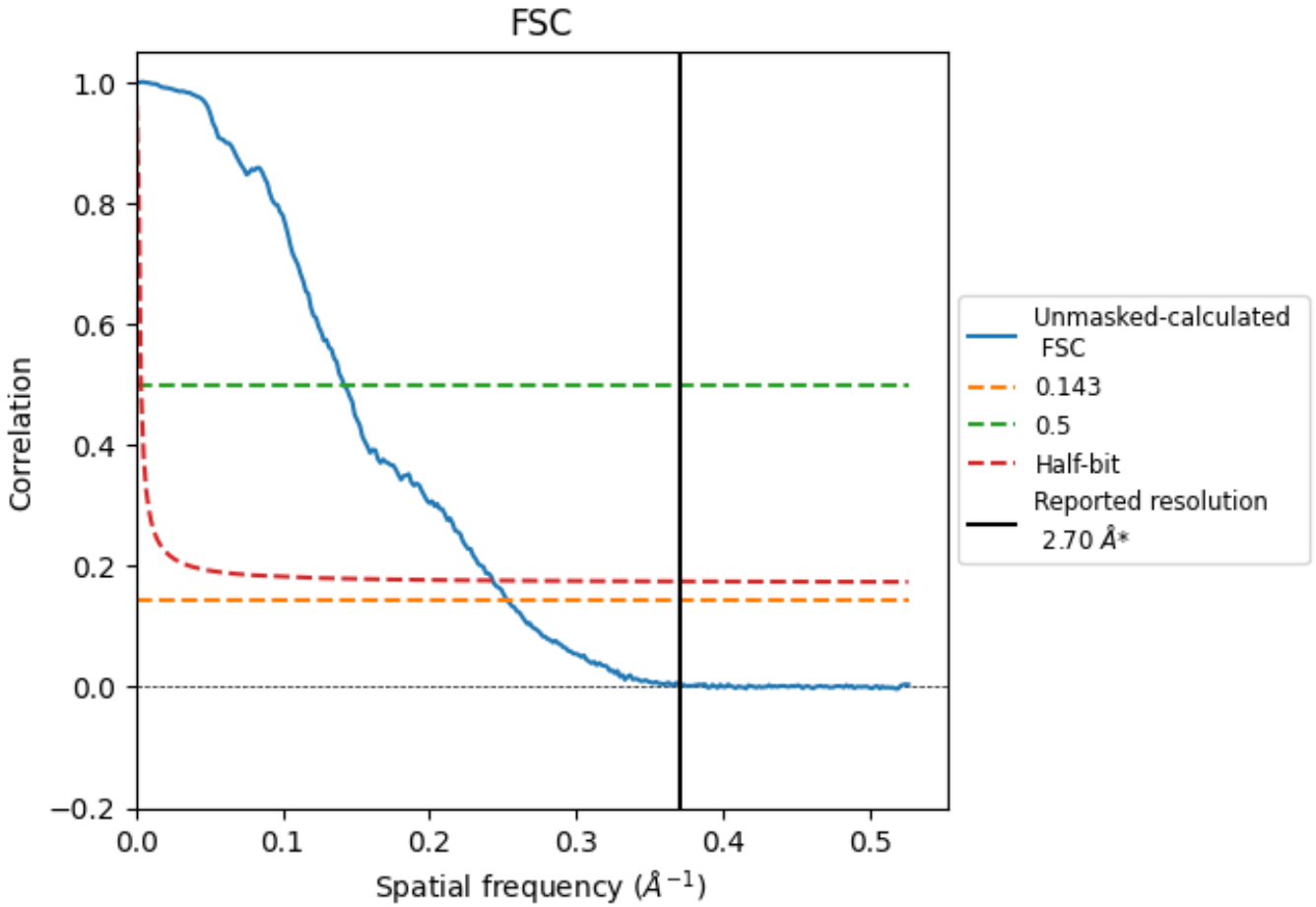


*Reported resolution corresponds to spatial frequency of 0.370 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8.2 Resolution estimates (i)

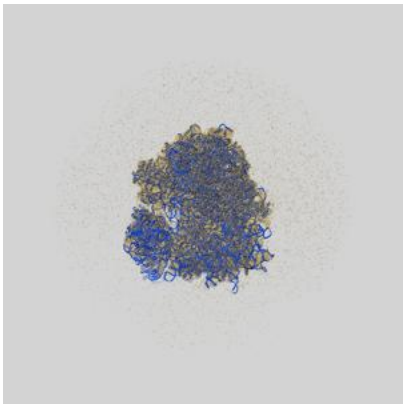
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.95	7.06	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 2.7 by more than 10 %

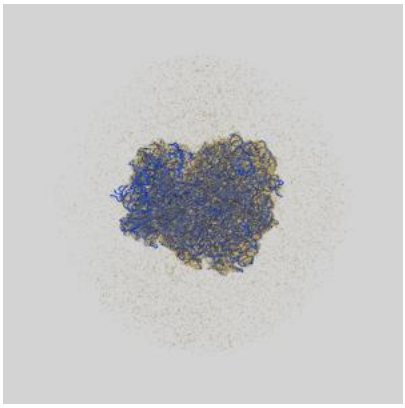
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-60088 and PDB model 8ZGR. Per-residue inclusion information can be found in section 3 on page 18.

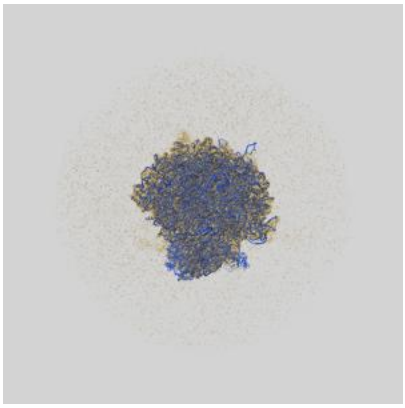
9.1 Map-model overlay



X



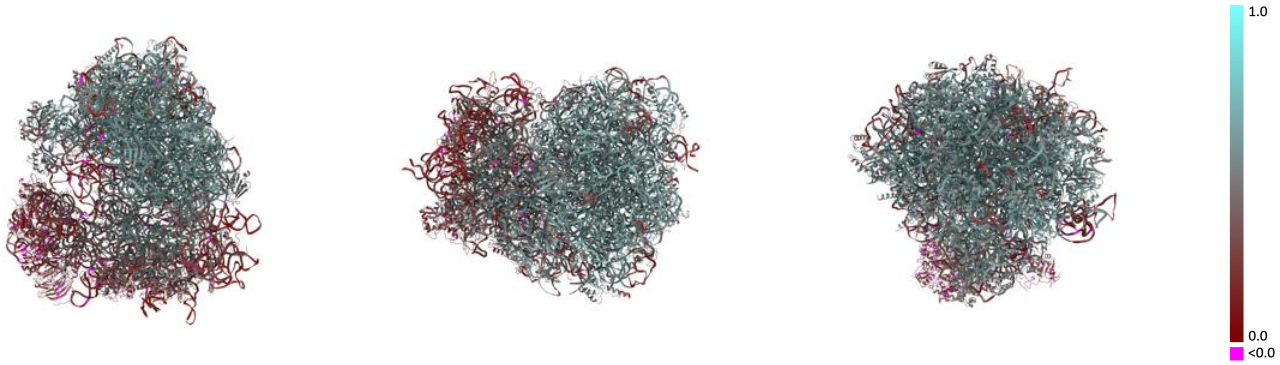
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

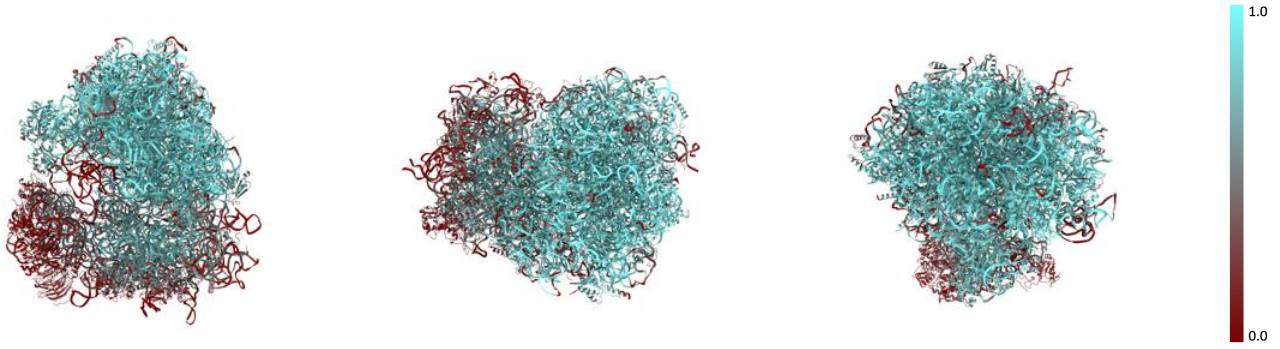
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

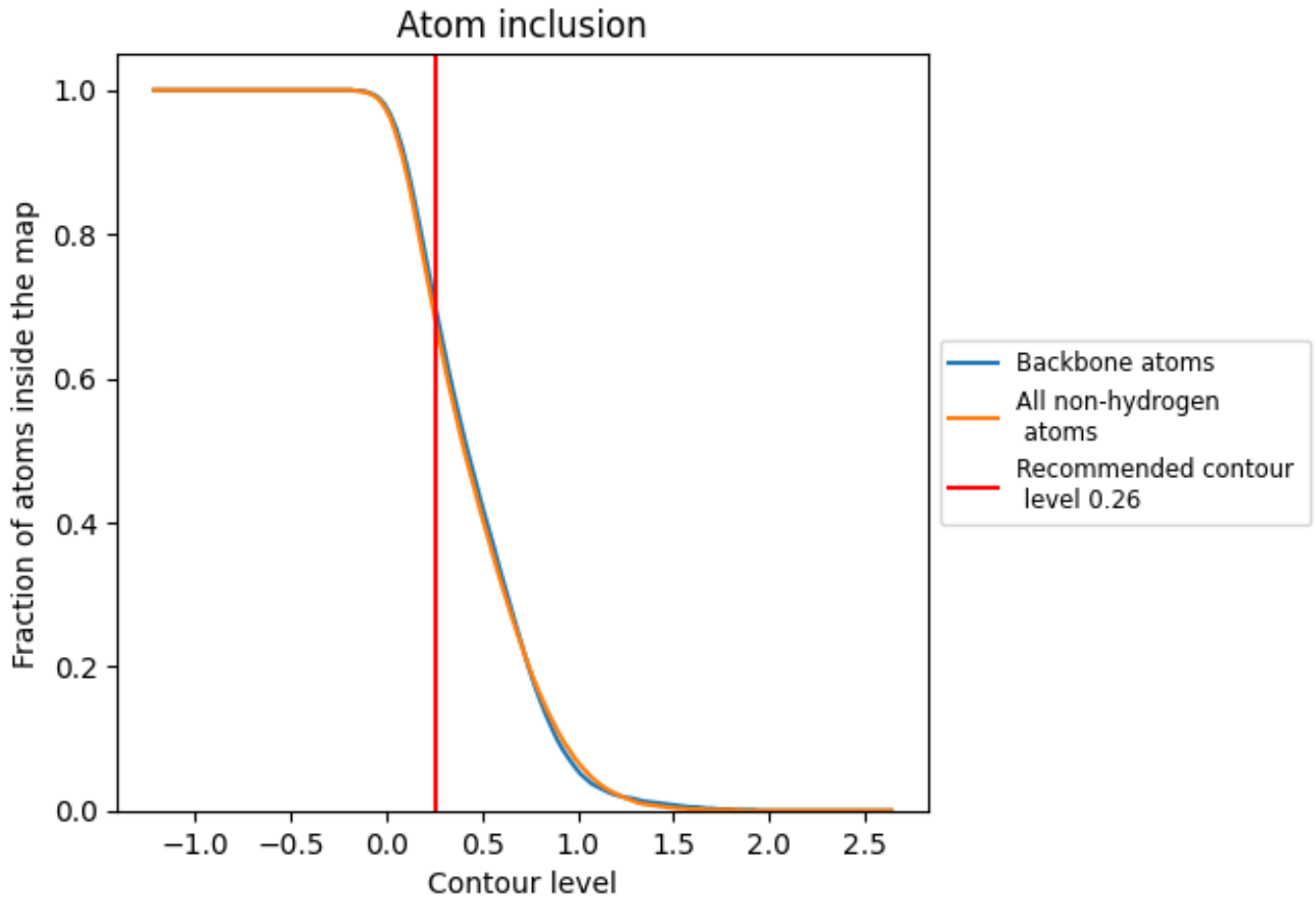
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.26).

9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6750	0.4660
LA	0.8560	0.5480
LB	0.8740	0.5350
LC	0.8870	0.5630
LD	0.9030	0.6170
LE	0.8760	0.5970
LF	0.8200	0.5610
LG	0.7300	0.5140
LH	0.7310	0.5170
LI	0.8730	0.5900
LJ	0.7470	0.5300
LK	0.7870	0.5560
LL	0.7950	0.5560
LM	0.6720	0.4850
LN	0.8120	0.5740
LO	0.8170	0.5600
LP	0.9080	0.6120
LQ	0.8690	0.5890
LR	0.8370	0.5970
LS	0.8700	0.5930
LT	0.7440	0.5360
LU	0.8700	0.5870
LV	0.8580	0.5880
LW	0.6650	0.4770
LX	0.8680	0.6000
LY	0.8710	0.5950
LZ	0.8150	0.5740
La	0.8290	0.5680
Lb	0.7670	0.5320
Lc	0.8710	0.5870
Ld	0.8360	0.5720
Le	0.7830	0.5550
Lf	0.8120	0.5670
Lg	0.7840	0.5520
Lh	0.9090	0.6170

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Chain	Atom inclusion	Q-score
Li	0.8180	0.5760
Lj	0.7970	0.5640
Lk	0.7740	0.5510
Ll	0.9320	0.6140
Lm	0.6080	0.4580
Ln	0.8700	0.5970
Lo	0.8410	0.5770
Lp	0.7310	0.5700
Lq	0.8310	0.5940
Lr	0.8010	0.5880
S2	0.5150	0.3330
SA	0.1560	0.2670
SB	0.1050	0.1940
SC	0.1220	0.2120
SD	0.0200	0.1490
SE	0.2130	0.2720
SF	0.1730	0.2630
SG	0.1570	0.2500
SH	0.1970	0.2560
SI	0.1670	0.2220
SJ	0.1500	0.2470
SK	0.0380	0.1490
SL	0.1400	0.2670
SM	0.3240	0.3470
SN	0.0240	0.1910
SO	0.0700	0.2050
SP	0.3840	0.3650
SQ	0.2510	0.2570
SR	0.4750	0.4110
SS	0.4690	0.4040
ST	0.3680	0.3810
SU	0.3360	0.3500
SV	0.6280	0.4770
SW	0.3720	0.3250
SX	0.6960	0.5150
SY	0.6040	0.4670
SZ	0.1710	0.1630
Sa	0.4410	0.3770
Sb	0.6780	0.5070
Sc	0.6330	0.5050
Sd	0.3350	0.3290
Se	0.4990	0.3600

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Chain	Atom inclusion	Q-score
Sf	0.4560	0.3950
Sg	0.3100	0.3190
Ta	0.0230	0.1620